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OM protein - protein search, using sw model

Run on:

December 10, 2003, 19:30:51 ; Search time 41 Seconds

(without alignments)

472.308 Million cell updates/sec

Title: US-09-897-645-1

Sequence: 1 MRMIVGHGIDIBLASSERSA.....1SHTDQFVTASVILEENHES 122

Scoring table: BLOSUM62

Gapext 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters:

1107863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing First 45 summaries

Database :

A_Geneseq_19JUN03:*

1: /SIDS1/gcdata/geneseq/geneseq/geneseq-emb1/AA1980.DAT:*

2: /SIDS1/gcdata/geneseq/geneseq/geneseq-emb1/AA1982.DAT:*

3: /SIDS1/gcdata/geneseq/geneseq/geneseq-emb1/AA1983.DAT:*

4: /SIDS1/gcdata/geneseq/geneseq/geneseq-emb1/AA1984.DAT:*

5: /SIDS1/gcdata/geneseq/geneseq/geneseq-emb1/AA1985.DAT:*

6: /SIDS1/gcdata/geneseq/geneseq-emb1/AA1986.DAT:*

7: /SIDS1/gcdata/geneseq/geneseq-emb1/AA1987.DAT:*

8: /SIDS1/gcdata/geneseq/geneseq-emb1/AA1988.DAT:*

9: /SIDS1/gcdata/geneseq/geneseq-emb1/AA1989.DAT:*

10: /SIDS1/gcdata/geneseq/geneseq-emb1/AA1990.DAT:*

11: /SIDS1/gcdata/geneseq/geneseq-emb1/AA1991.DAT:*

12: /SIDS1/gcdata/geneseq/geneseq-emb1/AA1992.DAT:*

13: /SIDS1/gcdata/geneseq/geneseq-emb1/AA1993.DAT:*

14: /SIDS1/gcdata/geneseq/geneseq-emb1/AA1994.DAT:*

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17: /SIDS1/gcdata/geneseq/geneseq-emb1/AA1997.DAT:*

18: /SIDS1/gcdata/geneseq/geneseq-emb1/AA1998.DAT:*

19: /SIDS1/gcdata/geneseq/geneseq-emb1/AA1999.DAT:*

20: /SIDS1/gcdata/geneseq/geneseq-emb1/AA2000.DAT:*

21: /SIDS1/gcdata/geneseq/geneseq-emb1/AA2001.DAT:*

22: /SIDS1/gcdata/geneseq/geneseq-emb1/AA2002.DAT:*

23: /SIDS1/gcdata/geneseq/geneseq-emb1/AA2003.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	% Match	Length	DB ID	Description
1	61.8	100.0	122	19	AAW80612	S. pneumoniae protein
2	61.8	100.0	122	22	AAU37879	Streptococcus pneumoniae
3	61.8	100.0	122	22	AAU38056	Streptococcus pneumoniae
4	61.8	100.0	156	21	AYY8388	S-YdcB essential
5	60.8	98.4	120	21	AYY58607	Streptococcus pneumoniae
6	60.8	98.4	120	24	AYU2175	S. pneumoniae type
7	33.9	54.9	118	23	ABP2726	Streptococcus poly
8	32.8	53.2	119	21	AYY91289	Group B Streptococcal
9	32.8	53.2	119	23	ABP27225	Streptococcus poly

ALIGNMENTS

RESULT 1	ID AAW80612	AAW80612 standard; Protein; 122 AA.
	XX	AAW80612;
	XX	DT 24-DEC-1998 (first entry)
	XX	S. pneumoniae protein of unknown function.
	XX	Streptococcus pneumoniae protein; recombinant; gene expression; DNA chip; virulence; antibody; infection; detection; treatment; hypothetical; Escherichia coli protein; Human EXMD-1 SEQ
	KW	Streptococcus pneumoniae protein; recombinant; gene expression; DNA chip; cell wall biosynthetic; external target; minimal gene set protein; Staphylococcus epidermidis protein
	KW	Streptococcus pneumoniae protein; recombinant; gene expression; DNA chip; cell wall biosynthetic; external target; minimal gene set protein; Staphylococcus epidermidis protein
	OS	Streptococcus pneumoniae
	XX	Streptococcus pneumoniae
	PN	W09826072-A1.
	XX	18-JUN-1998.
	XX	09-DEC-1997; 97W0-US22578.
	PR	13-DEC-1996; 96US-0036281.
	XX	(ELLI) LILLY & CO ELLI.
	XX	Baltz RH, Burgett SG, Dehoff BS, Hoskins JA, Jaskunas SR, Mills BJ, Norris FH, Peery RB, Rockey PK, Rosteck PR, Skarud PL, Smith MC, Solenberg PJ, Treadaway PJ, Young Bellido ML; WPI; 1998-340529/30.

DR N-PSDB; AAV65294.
 XX PT Haselbeck R, Ohlsen KL, Zyskind JW, Wall D, Trawick JD, Carr GJ;
 PT Yamamoto RT, Xu HH;
 PT XX WRI; 2001-011495/70.
 PT DR N-PSDB; AAC55738.
 XX PT New Polynucleotides for the identification and development of
 XX antibiotics, comprise sequences of antisense nucleic acids.
 XX Example 3; Seq ID No 13472; 51pp; English.
 CC The invention relates to antisense inhibitors of genes essential to
 CC prokaryotic cellular proliferation, their use in identifying the
 CC genes, their use in the discovery of novel antibiotics, the essential
 CC genes themselves and the encoded proteins. The prokaryotes used are
 CC Escherichia coli, Staphylococcus aureus, Salmonella typhi, Klebsiella
 CC pneumoniae, Pseudomonas aeruginosa and Enterococcus faecalis. The
 CC invention is also useful for the identification of potential new targets
 CC for antibiotic development. The antisense nucleic acids can also be used
 CC to identify proteins used in proliferation, to express these proteins,
 CC and to obtain antibodies capable of binding to the expressed proteins.
 CC The proteins can be used to screen compounds in rational drug discovery
 CC programme. The antisense nucleic acid sequence is also useful to screen
 CC for homologous nucleic acids which are required for cell proliferation in
 CC a wide variety of organisms. The present sequence represents an
 CC essential prokaryotic cellular proliferation protein.
 CC Note: The sequence data for this patent did not form part
 CC of the printed specification, but was obtained in electronic
 CC format directly from WIPO at
 CC [ftp.wipo.int/pub/published_pct_sequences](http://wipo.int/pub/published_pct_sequences).

SQ Sequence 122 AA;

Query Match 100.0%; Score 618; DB 19; Length 122;
 Best Local Similarity 100.0%; Pred. No. 2, 7e-69; Indels 0; Gaps 0;
 Matches 122; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRMIVGHGIDIELIASIESAVTRHGFAKVLTQEMERTSISKGRQLEYLAGRWSAKE 60
 Db 61 AFSKAMGIGISKLGFQDLEVNNERGAPYSQAFSGKWLSTSHTDQFTAVILENH 120
 61 AFSKAMGIGISKLGFQDLEVNNERGAPYSQAFSGKWLSTSHTDQFTAVILENH 120

Qy 121 ES 122
 Db 121 ES 122

RESULT 2

AAU37879 ID MRMIVGHGIDIELIASIESAVTRHGFAKVLTQEMERTSISKGRQLEYLAGRWSAKE 60
 AAU37879 XX
 AAU37879 AC
 AAU37879 DT 14-FEB-2002 (first entry)

XX DE Streptococcus pneumoniae cellular proliferation protein #308.
 KW Antisense; prokaryotic cellular proliferation protein;
 KW antibiotic; antibacterial; drug design.
 OS Streptococcus pneumoniae.

XX WO200170955-A2.

PN PR 21-MAR-2000; 2000US-191078P.
 PR 22-MAR-2000; 2000US-206848P.
 PR 23-MAY-2000; 2000US-207727P.
 PR 23-OCT-2000; 2000US-242578P.
 PR 27-NOV-2000; 2000US-253625P.
 PR 22-DEC-2000; 2000US-25791P.
 PR 16-FEB-2001; 2001US-269308P.
 XX PA (ELIT-) ELITRA PHARM INC.
 XX

PR Haselbeck R, Ohlsen KL, Zyskind JW, Wall D, Trawick JD, Carr GJ;
 PI Yamamoto RT, Xu HH;
 PR XX WRI; 2001-011495/70.
 PR DR N-PSDB; AAC55738.

PT New Polynucleotides for the identification and development of
 XX antibiotics, comprise sequences of antisense nucleic acids.
 XX Example 3; Seq ID No 13472; 51pp; English.
 CC The invention relates to antisense inhibitors of genes essential to
 CC prokaryotic cellular proliferation, their use in identifying the
 CC genes, their use in the discovery of novel antibiotics, the essential
 CC genes themselves and the encoded proteins. The prokaryotes used are
 CC Escherichia coli, Staphylococcus aureus, Salmonella typhi, Klebsiella
 CC pneumoniae, Pseudomonas aeruginosa and Enterococcus faecalis. The
 CC invention is also useful for the identification of potential new targets
 CC for antibiotic development. The antisense nucleic acids can also be used
 CC to identify proteins used in proliferation, to express these proteins,
 CC and to obtain antibodies capable of binding to the expressed proteins.
 CC The proteins can be used to screen compounds in rational drug discovery
 CC programme. The antisense nucleic acid sequence is also useful to screen
 CC for homologous nucleic acids which are required for cell proliferation in
 CC a wide variety of organisms. The present sequence represents an
 CC essential prokaryotic cellular proliferation protein.
 CC Note: The sequence data for this patent did not form part
 CC of the printed specification, but was obtained in electronic
 CC format directly from WIPO at
 CC [ftp.wipo.int/pub/published_pct_sequences](http://wipo.int/pub/published_pct_sequences).

SQ Sequence 122 AA;

Query Match 100.0%; Score 618; DB 22; Length 122;
 Best Local Similarity 100.0%; Pred. No. 2, 7e-69; Indels 0; Gaps 0;
 Matches 122; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRMIVGHGIDIELIASIESAVTRHGFAKVLTQEMERTSISKGRQLEYLAGRWSAKE 60
 Db 61 AFSKAMGIGISKLGFQDLEVNNERGAPYSQAFSGKWLSTSHTDQFTAVILENH 120
 61 AFSKAMGIGISKLGFQDLEVNNERGAPYSQAFSGKWLSTSHTDQFTAVILENH 120

Qy 121 ES 122
 Db 121 ES 122

RESULT 3

AAU38056 ID MRMIVGHGIDIELIASIESAVTRHGFAKVLTQEMERTSISKGRQLEYLAGRWSAKE 60
 AAU38056 XX
 AAU38056 AC
 AAU38056 DT 14-FEB-2002 (first entry)

XX DE Streptococcus pneumoniae cellular proliferation protein #485.
 KW Antisense; prokaryotic cellular proliferation protein;
 KW antibiotic; antibacterial; drug design.

XX WO200170955-A2.

PR 27-SEP-2001.

PR 21-MAR-2001; 2001WO-US09180.

PR 23-MAY-2000; 2000US-206848P.

PR 26-MAY-2000; 2000US-207727P.

PR 23-OCT-2000; 2000US-242578P.

PR 27-NOV-2000; 2000US-253625P.

PR 22-DEC-2000; 2000US-25791P.

PR 16-FEB-2001; 2001US-269308P.

XX PA (ELIT-) ELITRA PHARM INC.

XX

PR 26-MAY-2000; 2000US3-207727P.
 PR 23-OCT-2000; 2000US-242578P.
 PR 27-NOV-2000; 2000US-253625P.
 PR 22-DEC-2000; 2000US-257931P.
 PR 16-FEB-2001; 2001US-269308P.
 PA (ELIF-) ELUTRA PHARM INC.
 XX Haselbeck R, Ohlsen KL, Zyskind JW, Wall D, Trawick JD, Carr GU;
 PI Yamamoto RT, Xu HH;
 XX WPI; 2001-611435/70.
 DR N-PSB; AAS55915.
 XX New polynucleotides for the identification and development of
 PT antibiotics, comprise sequences of antisense nucleic acids -
 XX Example 3; Seq ID No 13649; 51pp; English.
 XX The invention relates to antisense inhibitors of genes essential to
 CC prokaryotic cellular proliferation, their use in identifying the
 CC genes, their use in the discovery of novel antibiotics, the essential
 CC genes themselves and the encoded proteins. The prokaryotes used are
 CC *Escherichia coli*, *Staphylococcus aureus*, *Salmonella typhi*, *Klebsiella*
 CC *pneumoniae*, *Pseudomonas aeruginosa* and *Enterococcus faecalis*. The
 CC invention is also useful for the identification of potential new targets
 CC for antibiotic development. The antisense nucleic acids can also be used
 CC to identify proteins used in proliferation, to express these proteins,
 CC and to obtain antibodies capable of binding to the expressed proteins.
 CC The proteins can be used to screen compounds in rational drug discovery
 CC programmes. The antisense nucleic acid sequence is also useful to screen
 CC for homologous nucleic acids which are required for cell proliferation in
 CC a wide variety of organisms. The present sequence represents an
 CC essential prokaryotic cellular proliferation protein.
 CC Note: The sequence data for this patent did not form part
 CC of the printed specification, but was obtained in electronic
 CC format directly from WIPO at
 CC ftp://wipo.int/pub/published_pct_sequences.
 XX Sequence 122 AA;
 SQ Query Match 100.0%; score 618; DB 22; Length 122;
 Best Local Similarity 100.0%; Pred. No. 2.7e-69; Mismatches 0;
 Matches 122; Conservative 0; MisMatches 0; Indels 0; Gaps 0;
 QY 1 MRNIVGHGIDIEBLASIESAVRHEGAKRVLTAQEMERTFSIKGKQRIEYLAGRWSAKE 60
 Db 1 MRNIVGHGIDIEBLASIESAVRHEGAKRVLTAQEMERTFSIKGKQRIEYLAGRWSAKE 60
 QY 61 AFSKAMGTGISKLGFQDLEVNANNERGAPYFSQAPFSGKWLISHTDQFVTASVILENH 120
 Db 61 AFSKAMGTGISKLGFQDLEVNANNERGAPYFSQAPFSGKWLISHTDQFVTASVILENH 120
 QY 61 AFSKAMGTGISKLGFQDLEVNANNERGAPYFSQAPFSGKWLISHTDQFVTASVILENH 120
 Db 121 ES 122
 QY 121 ES 122
 Db 121 ES 122
 RESULT 4
 AAY8388
 ID AAY8388 standard; Protein; 156 AA.
 AC AAY8388;
 XX DT 25-JUL-2000 (first entry)
 XX S_ydcB essential bacterial protein amino acid sequence.
 XX
 XX Bacteria; S-ydcB; Streptococcus pneumoniae; antibacterial compound;
 KW acyl carrier protein synthase; identify; bacterial infection; treatment.
 OS Streptococcus pneumoniae.
 XX
 PN WO9961452-A2.
 XX PD 02-DEC-1999.

PN WO20018952-A1.
 XX 06-APR-2000.
 PD XX
 AC XX
 AC 30-SEP-1999; 99WO-US22666.
 KW XX
 PR 30-SEP-1998; 98US-0163446.
 PA (MILL-) MILLENNIUM PHARM INC.
 XX PI Fritz C, Youngman P, Guzman L;
 XX DR WPI; 2000-303457/26.
 DR N-PSB; AAA13270.
 XX PS Claim 17; Fig 1; 58pp; English.
 XX PT Identifying new antibacterial agents particularly against *Streptococcus*
 PT pneumoniae, uses S-YdcB polypeptide from *S. pneumoniae* and B-YdcB
 PT polypeptide from *Bacillus subtilis* -
 XX PS
 CC This sequence represents the protein encoded by the essential bacterial
 CC gene S-YdcB from *Streptococcus pneumoniae*. B-YdcB is an S-YdcB ortholog
 CC from *Bacillus subtilis*. The gene encodes a protein which has structural
 CC characteristics of acyl carrier protein synthase and displays synthase
 CC activity in vitro. The protein is used in a method for identifying an
 CC antibacterial agent, which comprises contacting an S-YdcB or B-YdcB
 CC polypeptide with a test compound and detecting an interaction between the
 CC polypeptide and the test compound, where the interaction indicates that
 CC the compound is an antibacterial compound. Antibacterial agents
 CC identified using the method may be used to treat a bacterial infection,
 CC especially *Streptococcus pneumoniae* in mammals, especially a human or
 CC rodent. The method can be configured for high throughput screening of
 CC numerous candidate antibacterial agents, and identified agents should
 CC have a broad spectrum of antibacterial activity.
 XX SQ Sequence 156 AA;
 Query Match 100.0%; score 618; DB 21; Length 156;
 Best Local Similarity 100.0%; Pred. No. 3.8e-69; Mismatches 0;
 Matches 122; Conservative 0; MisMatches 0; Indels 0; Gaps 0;
 QY 1 MRNIVGHGIDIEBLASIESAVRHEGAKRVLTAQEMERTFSIKGKQRIEYLAGRWSAKE 60
 Db 35 MRNIVGHGIDIEBLASIESAVRHEGAKRVLTAQEMERTFSIKGKQRIEYLAGRWSAKE 94
 QY 61 AFSKAMGTGISKLGFQDLEVNANNERGAPYFSQAPFSGKWLISHTDQFVTASVILENH 120
 Db 95 AFSKAMGTGISKLGFQDLEVNANNERGAPYFSQAPFSGKWLISHTDQFVTASVILENH 154
 QY 121 ES 122
 Db 155 ES 156
 RESULT 5
 AAY58607
 ID AAY58607 standard; Protein; 120 AA.
 AC AAY58607;
 XX DT 11-APR-2000 (first entry)
 DE Streptococcus pneumoniae acyl carrier protein synthase acps.
 KW Acyl carrier protein synthase; acps; infection; therapy;
 KW diagnosis; antibacterial; antibiotic; Helicobacter pylori.
 OS Streptococcus pneumoniae.
 KW PN WO9961452-A2.
 XX PD 02-DEC-1999.

XX	27-MAY-1999;	99WO-US11704.
PF		
XX	28-MAY-1998;	98US0-0087079.
PR		
XX		
PA	(SMIK) SMITHKLINE BEECHAM CORP.	
XX		
PI	Pearson SC, Kallender H;	
XX		
DR	WPI; 2000-147027/13.	
XX		
PS	N-PSDB; AA225350.	
XX		
PT	New isolated Streptococcus pneumoniae acps polypeptides, used to develop products for treating, e.g. otitis media -	
XX		
CC	Claim 1, Page 31-32; 34pp; English.	
XX		
CC	The present sequence represents the acps protein of Streptococcus pneumoniae strain 010993 (NCIM 4094), which is phylogenetically related to proteins of the acyl carrier protein synthase family. The invention provides acps polypeptides having at least 70% identity with the present sequence, as well as acps polynucleotides, recombinant materials and methods for their production. The polypeptides and polynucleotides can be used for the diagnosis, prognosis or treatment of a disease related to the expression or activity of acps. They can be used to treat microbial diseases such as bacterial infections, particularly S. pneumoniae infections, to prevent infections and to identify agonists and antagonists useful as antibacterial compounds. They can also be used to prevent bacterial adhesion to mammalian, extracellular matrix proteins on indwelling devices or to extracellular matrix proteins in wounds, to block bacterial adhesion between mammalian, extracellular matrix proteins and bacterial acps proteins that mediate tissue damage and/or to block the normal progression of pathogenesis in infections other than by the implantation of in-dwelling devices or by other surgical techniques. The antibacterial compounds can be used in the treatment of Helicobacter pylori (HP) infections, to decrease the advent of HP-induced cancers, such as gastrointestinal carcinoma, and also to prevent, inhibit and/or cure gastric ulcer and gastritis. They can also be used for treating e.g. otitis media, conjunctivitis, pneumonia, bacteraemia, meningitis, sinusitis, pleural empyema and endocarditis.	
XX		
SQ	Sequence 120 AA;	
Query Match	98.4%; Score 608; DB 21; Length 120;	
Best Local Similarity	100.0%; Pred. 4.7e-68;	
Matches	120; Conservative 0; Mismatches 0; Indels 0; Gaps 0	
QY	3 MIVGHGIDIERLAS ESAVTREHGFAKRVLTQAEWMRFTSIKGRRQTEYLAGRWSAKEAF 62	
Db	1 MIVGHGIDIERLAS ESAVTREHGFAKRVLTQAEWMRFTSIKGRRQTEYLAGRWSAKEAF 60	
QY	63 SKAMMGTGISKLGQDDEVLNNEERGAPFSQAFPSKGKWLISHTDQFTVASTVILEENHES 122	
Db	61 SKAMMGTGISKLGQDDEVLNNEERGAPFSQAFPSKGKWLISHTDQFTVASTVILEENHES 120	
RESULT 6		
ABU02175		
ID	ABU02175 standard; Protein; 120 AA.	
XX		
AC		
XX		
ABU02175;		
XX		
DT	11-FEB-2003 (first entry)	
XX		
DE	S. pneumoniae type 4 strain protein from coding region #1752.	
KW	Bacterial meningitis; pneumonia; sepsis; otitis media;	
KW	ear infection; antiinflammatory; antibacterial; immunostimulant;	
KW	auditory; respiratory; gene therapy; vaccine.	
XX		

OS Streptococcus pneumoniae type 4 strain:
XX WO200277021-A2.
PN XX
XX PD 03-OCT-2002.
PF XX 27-MAR-2002; 2002WO-IB02163.
XX PR XX 27-MAR-2001; 2001GB-0007658.
PA XX
PA (CHIR-) CHIRON SPA;
PA (GENO-) INST GENOMIC RES.
PA XX
PI XX Masignani V, Tettelin H, Fraser C;
DR XX WPI: 2003-040579/03.
N-SSDB; ABX07464.
PT XX
PT XX New proteins and nucleic acid molecules from *Streptococcus pneumoniae*,
PT useful as medicaments for treating or preventing a disease or infection
PT due to *streptococcus* bacteria, such as pneumonia, sepsis, otitis media
PT or ear infection -
XX
PS XX
Claim 1; SEQ ID NO 3504; 56pp; English.
CC
CC The invention relates to a protein comprising or having at least 50%
CC identity to any of the 2469 amino acid sequences, identified in the
CC specification (available on a computer readable format), or its fragment,
CC expressed from 2469 of 2489 identified DNA coding regions from the
CC *Streptococcus pneumoniae* type 4 strain genomic sequence appearing as
CC ABS6454. Also included are an antibody which binds one of the
CC proteins, treating a patient by administering the protein, DNA or
CC antibody (in a composition), a kit comprising first and second primers,
CC which are the nucleic acid cited above or fragments between nucleotides
CC 8-100 of a sequence not defined in the specification, for amplifying a
CC target sequence contained within a *Streptococcus* nucleic acid sequence,
CC where the first primer is substantially complementary to the target
CC sequence and the second primer is substantially complementary to the
CC complement of the target sequence, and where the parts of the primers
CC having substantial complementarity define the termini of the target
CC sequence to be amplified, assay comprising contacting a test compound
CC with the protein, and determining whether the test compound binds to the
CC protein and a *Streptococcus pneumoniae* bacterium, where one or more
CC genes encoding the protein has been rendered inactive. The proteins,
CC nucleic acid molecules, antibody and compositions are useful as
CC medicaments for treating or preventing a disease or infection due to
CC *streptococcus* bacteria, particularly *S. pneumoniae*, such as pneumonia,
CC sepsis, otitis media or ear infection. They are also useful in developing
CC vaccines, diagnostics and antibiotics. The methods are useful for
CC identifying immunodominant proteins. The present sequence is one of
CC the 2469 proteins expressed by the identified coding regions from the
CC genomic sequence.
CC
Note: The sequence data for this patent did not form part
CC of the printed specification, but was obtained in electronic
CC format directly from WIPO at
CC ftp://wipo.int/pub/published_pct_sequences.
XX
Sequence 120 AA;

ABP27226
ID ABP27226 standard; Protein; 118 AA.
XX
AC ABP27226;
XX DT 02-JUL-2002 (first entry)
XX DE Streptococcus polypeptide SEQ ID NO 3628.
XX KW Streptococcus; GAS; GBS; group B streptococcus; Streptococcus agalactiae;
group A streptococcus; Streptococcus pyogenes; antibacterial;
antiinflammatory; infection; vaccine; meningitis; gene therapy.
XX OS Streptococcus pyogenes.
XX OS Streptococcus agalactiae.
XX PN WO200234771-A2.
XX PD 02-MAY-2002.
XX PF 29-OCT-2-2001; 2001WO-GB04789.
XX PR 27-OCT-2000; 2000GB-0026333.
XX PR 24-NOV-2000; 2000GB-0028727.
XX PR 07-MAR-2001; 2001GB-0005640.
XX PA (CHIR-) CHIRON SPA.
PA (GENO-) INST GENOMIC RES.
XX Telford J, Masianni V, Margarit Ros YI, Grandi G, Fraser C,
PI Tettelin H,
XX WPI; 2002-3-22536/38.
DR ABN67857.
XX DR ABN67857.
PT New Streptococcus protein for the treatment or prevention of infection
PT or disease caused by Streptococcus bacteria, such as meningitis, and
PT for detecting a compound that binds to the protein -
XX Claim 1; Page 3517; 4525pp; English.
The invention relates to a protein (ABP25413-ABP30895) from group B
streptococcus/GBS (Streptococcus agalactiae) or group A streptococcus/GAS
(Streptococcus pyogenes), comprising one of 5483 sequences (S1), given in
the specification. The proteins have antibacterial and antiinflammatory
activity. (I), nucleic acids encoding (I), ABN6044-ABN71526 and
antibodies that bind (I) are used in the manufacture of medicaments for
the treatment or prevention of infection or disease caused by
Streptococcus bacteria, particularly *S. agalactiae* and *S. pyogenes*.
Nucleic acids encoding (I) are used to detect Streptococcus in a
biological sample. (I) is used to determine whether a compound binds to
(I). A composition comprising (I) or a nucleic acid encoding (I), may be
used as a vaccine or diagnostic composition. The disease caused by
Streptococcus that is prevented or treated may be meningitis. Nucleic
acid encoding (I) may be used to recombinantly produce (I) and may be
used in gene therapy. Antibodies to (I) are used for affinity
chromatography, immunoassays, and distinguishing/identifying
Streptococcus proteins.
XX Sequence 118 AA;
Query Match 54.9%; Score 339; DB 23; Length 118;
Best Local Similarity 53.4%; Pred. No. 2.5e-34; Mismatches 27; Indels 0; Gaps 0;
Matches 62; Conservative 52.1%; Pred. No. 5.3e-33;
QY 3 MIVGHGIDDEELASIESAVTRHEGAKRILTAQEMERFFSLKGRQIEVLAGRWSAKAF 62
Db 1 MIVGHGIDDEELASIESAVTRHEGAKRILTAQEMERFFSLKGRQIEVLAGRWSAKAF 60
QY 3 SKAMGTGSKLQGDLLEVNERRGAPYSQAPSQPKWISLISHTDQFTAVSLEE 118
Db 1 MIVGHGIDDEELASIESAVTRHEGAKRILTAQEMERFFSLKGRQIEVLAGRWSAKAF 61
QY 62 FSKAMGTGSKLQGDLLEVNERRGAPYSQAPSQPKWISLISHTDQFTAVSLEE 118
Db 61 YSKALGTGIGKVNPHDIEILSDDKGAPLITKPEKGSKFVSHSGNYAQASVILE 117
RESULT 9
ABP27225
ID ABP27225 standard; Protein; 119 AA.
XX AC ABP27225;
XX DT 02-JUL-2002 (first entry)
XX DE Streptococcus polypeptide SEQ ID NO 3626.
XX KW Streptococcus; GAS; GBS; group B streptococcus; Streptococcus agalactiae;

KW group A streptococcus; streptococcus pyogenes; meningitis; gene therapy.
 KW antiinflammatory; infection; vaccine; menigitis; gene therapy.
 XX
 OS Streptococcus agalactiae.
 XX
 PN WO200234771-A2.
 XX
 PD 02-MAY-2002.
 XX
 PF 29-OCT-2001; 2001WO-GB04789.
 XX
 PR 27-OCT-2000; 2000GB-0026333.
 PR 24-NOV-2000; 2000GB-0028727.
 PR 07-MAR-2001; 2001GB-0005640.
 XX
 PA (CHTR-) CHIRON SPA.
 PA (GENO-) INST GENOMIC RES.
 XX
 PI Telford J, Masianni V, Margarit Ros YI, Grandi G, Fraser C;
 PI Tettelin H;
 XX
 DR WPI; 2002-352536/38.
 XX
 PT New Streptococcus protein for the treatment or prevention of infection or disease caused by Streptococcus bacteria, such as meningitis, and for detecting a compound that binds to the protein.
 XX
 PS Claim 1; Page 3516; 4525pp; English.
 XX
 CC The invention relates to a protein (ABP25413-ABP30895) from group B streptococcus (GBS (streptococcus agalactiae) or group A streptococcus/GAS (Streptococcus pyogenes), comprising one of 543 sequences (S1), given in the specification. The proteins have antibacterial and antiinflammatory activity. (1) nucleic acids encoding (1), ABN6044-ABN71226 and antibodies that bind (1) are used in the manufacture of medicaments for the treatment or prevention of infection or disease caused by Streptococcus bacteria, particularly S. agalactiae and S. pyogenes.
 CC Nucleic acids encoding (1) are used to detect Streptococcus in a biological sample. (1) is used to determine whether a compound binds to (1). A composition comprising (1) or a nucleic acid encoding (1), may be used as a vaccine or diagnostic composition. The disease caused by Streptococcus that is prevented or treated may be meningitis. Nucleic acid encoding (1) may be used to recombinantly produce (1) and may be used in gene therapy. Antibodies to (1) are used for affinity chromatography, immunoassays, and distinguishing/identifying Streptococcus proteins.
 CC
 Sequence 119 AA;
 Query Match 53.2%; Score 328.5; DB 23; Length 119;
 Best Local Similarity 52.1%; Pred. No. 5.3e-33;
 Matches 61; Conservative 29; Mismatches 26; Indels 1; Gaps 1;
 XX
 Qy 3 MIVGHGIDIEBLASLATESAVIRHEGFKRVRVITAQEMERFTSUGK-KRQEYLAGRNSAKEA 61
 Db 1 MIVGHGIDIEBLASLATESAVIRHEGFKRVRVITAQEMERFTSUGK-KRQEYLAGRNSAKEA 60
 Qy 3 MIVGHGIDIEBLASLATESAVIRHEGFKRVRVITAQEMERFTSUGK-KRQEYLAGRNSAKEA 61
 Db 1 MIVGHGIDIEBLASLATESAVIRHEGFKRVRVITAQEMERFTSUGK-KRQEYLAGRNSAKEA 60
 Qy 62 FSKAMGTGISK-LGQDLEVLANNERGAPFSQASPGSKWILSISHTDQFTIASVILEEN 119
 Db 61 FSKAMGTGISK-LGQDLEVLANNERGAPFSQASPGSKWILSISHTDQFTIASVILEEN 119
 Sequence 119 AA;
 Query Match 48.9%; Score 302; DB 23; Length 119;
 Best Local Similarity 51.3%; Pred. No. 1.1e-29;
 Matches 61; Conservative 25; Mismatches 31; Indels 2; Gaps 2;
 XX
 Qy 3 MIVGHGIDIEBLASLATESAVIRHEGFKRVRVITAQEMERFTSUGK-KRQEYLAGRNSAKEA 61
 Db 1 MIVGHGIDIEBLASLATESAVIRHEGFKRVRVITAQEMERFTSUGK-KRQEYLAGRNSAKEA 60
 Qy 62 FSKAMGTGISK-LGQDLEVLANNERGAPFSQASPGSKWILSISHTDQFTIASVILEEN 119
 Db 61 FSKAMGTGISK-LGQDLEVLANNERGAPFSQASPGSKWILSISHTDQFTIASVILEEN 119
 Sequence 119 AA;
 RESULT 10
 ABB54157 standard; Protein; 119 AA.
 XX
 AC ABB54157;
 XX
 DT 16-MAY-2002 (first entry)
 XX
 DB Lactococcus lactis protein acPS.
 XX
 KW Biosynthesis; biodegradation; lactic bacterium; yogurt; cheese.
 XX
 OS Lactococcus lactis IL1403.
 XX
 PN FR2807446-A1.
 XX
 PD 12-OCT-2001.
 XX
 PF 11-APR-2000; 2000FR-0004630.
 XX
 PR 11-APR-2000; 2000FR-0004630.
 XX
 PA (INRG) INRA INST NAT RECH AGRONOMIQUE.
 XX
 PI Bolotine A, Sorokine A, Renault P, Ehrlich SD;
 DR WPI; 2002-043418/05.
 XX
 PT New nucleotide sequence useful in the identification of Lactococcus lactis and related species -
 XX
 CC
 The present invention is related to a Lactococcus lactis nucleotide sequence (ABAB0521) and related proteins (ABB5330-ABB55621). The nucleic acid sequence is useful in the detection and/or amplification of nucleic acid sequence, particularly to identify Lactococcus lactis or related species. The proteins of the invention are useful for the biosynthesis or biodegradation of a composition of interest. The invention helps research in lactic bacteria, particularly useful in the production of yogurt and cheese.
 CC Note: The sequence data for this patent is based on equivalent patent WO20017334 (published 18-Oct-2001) which is available in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
 CC
 Sequence 119 AA;
 Query Match 48.9%; Score 302; DB 23; Length 119;
 Best Local Similarity 51.3%; Pred. No. 1.1e-29;
 Matches 61; Conservative 25; Mismatches 31; Indels 2; Gaps 2;
 XX
 Qy 3 MIVGHGIDIEBLASLATESAVIRHEGFKRVRVITAQEMERFTSUGK-KRQEYLAGRNSAKEA 61
 Db 1 MIVGHGIDIEBLASLATESAVIRHEGFKRVRVITAQEMERFTSUGK-KRQEYLAGRNSAKEA 60
 Qy 62 FSKAMGTGISK-LGQDLEVLANNERGAPFSQASPGSKWILSISHTDQFTIASVILEEN 119
 Db 61 FSKAMGTGISK-LGQDLEVLANNERGAPFSQASPGSKWILSISHTDQFTIASVILEEN 119
 Sequence 119 AA;

PR 26-MAY-2000; 2000US-207727P.
 PR 23-OCT-2000; 2000US-242579P.
 PR 27-NOV-2000; 2000US-253625P.
 PR 22-DEC-2000; 2000US-25731P.
 PR 16-FEB-2001; 2001US-26930BP.
 XX
 PA (ELIT-) ELTRA PHARM INC.
 XX Haselbeck R, Ohlsen KL, Zyskind JW, Wall D, Trawick JD, Carr GJ;
 PI PI Yamamoto RT, Xu HH;
 XX DR WPI; 2001-611495/70.
 XX N-PSDB; AAS53042.
 XX PT New polynucleotides for the identification and development of
 PT antibiotics, comprise sequences of antisense nucleic acids -
 XX Example 3; Seq ID No 10776; 51pp; English.
 XX PS The invention relates to antisense inhibitors of genes essential to
 CC prokaryotic cellular proliferation, their use in identifying the
 CC genes, their use in the discovery of novel antibiotics, the essential
 CC genes themselves and the encoded proteins. The prokaryotes used are
 CC Escherichia coli, Staphylococcus aureus, Salmonella typhi, Klebsiella
 CC pneumoniae, Pseudomonas aeruginosa and Enterococcus faecalis. The
 CC invention is also useful for the identification of potential new targets
 CC for antibiotic development. The antisense nucleic acids can also be used
 CC to identify proteins used in proliferation, to express these proteins,
 CC and to obtain antibodies capable of binding to the expressed proteins.
 CC The proteins can be used to screen compounds in rational drug discovery
 CC programmes. The antisense nucleic acid sequence is also useful to screen
 CC for homologous nucleic acids which are required for cell proliferation in
 CC a wide variety of organisms. The present sequence represents an
 CC essential prokaryotic cellular proliferation protein.
 CC Note: The sequence data for this patent did not form part
 CC of the printed specification, but was obtained in electronic
 CC format directly from WIPO at
 XX ftp.wipo.int/pub/published_pct_sequences.
 XX SQ Sequence 117 AA;
 Query Match 48.7%; Score 301; DB 22; length 117;
 Best Local Similarity 51.3%; Pred. No. 1; 5e-29; Mismatches 35; Indels 0; Gaps 0;
 Matches 59; Conservative 21; Mismatches 35; Indels 0; Gaps 0;
 Qy 3 MIVGHHGIDIEELASIESAVTRHEGFAKVLTAQEMERPTSLKGRRIQLEYLAGRWSAKEAF 62
 Db 1 MTKGIGIDATELKRRIASMAGRQKRAFAERILTRSELDDQYELSEBKRNKFPLAGRFAKEAF 60
 Qy 63 SIKMGTGISKLGQDIEVLRNNGAPFSQPSKGKWLISLGHQDQVTAASIL 116
 Db 61 SKAWGTGIGKGVQGLQDIEVLTKEKGAPVWVANSPHNGKVFSICHTDTWAIQVLE 115
 RESULT 12
 AAY8389 ID AAY8389 standard; Protein; 121 AA.
 XX AC AAY8389;
 XX DT 25-JUL-2000 (first entry)
 XX DE B-ydcB essential bacterial protein amino acid sequence.
 KW Bacterial gene; B-ydcB; Streptococcus pneumoniae; antibacterial compound;
 KW acyl carrier protein synthase; identify; bacterial infection; treatment;
 XX OS Bacillus subtilis.
 XX WO200018952-A1.
 XX PN 06-APR-2000.
 XX PR 30-SEP-1999; 99WO-US22666.
 XX PR 30-SEP-1998; 98US-0163446.
 XX PA (MILL-) MILLENIUM PHARM INC.
 XX PT Fritz C, Youngman P, Guzman L;
 XX DR WPI; 2000-303457/26.
 XX N-PSDB; AAA13271.
 XX PT Identifying new antibacterial agents particularly against *Streptococcus*
 PT *pneumoniae*, uses S-ydcB polypeptide from *S. pneumoniae* and B-ydcB
 XX polypeptide from *Bacillus subtilis* -
 PS Claim 17; Fig 2; 58pp; English.
 XX CC This sequence represents the essential bacterial protein B-ydcB from
 CC *Bacillus subtilis*. B-ydcB is an ortholog of the S-ydcB from *Streptococcus*
 CC *pneumoniae*. The gene encodes a protein which has structural
 CC characteristics of acyl carrier protein synthase and displays synthase
 CC activity in vitro. The protein is used in a method for identifying an
 CC antibacterial agent, which comprises contacting an S-ydcB or B-ydcB
 CC polypeptide with a test compound and detecting an interaction between the
 CC polypeptide and the test compound, where the interaction indicates that
 CC the compound is an antibacterial compound. Antibacterial agents
 CC identified using the method may be used to treat a bacterial infection,
 CC especially *Streptococcus pneumoniae* in mammals, especially a human or
 CC rodent. The method can be configured for high throughput screening of
 CC numerous candidate antibacterial agents, and identified agents should
 CC have a broad spectrum of antibacterial activity.
 XX SQ Sequence 121 AA;
 Query Match 40.6%; Score 251; DB 21; length 121;
 Best Local Similarity 44.6%; Pred. No. 2; 9e-23; Mismatches 32; Indels 10; Gaps 3;
 Matches 54; Conservative 25; Mismatches 32; Indels 10; Gaps 3;
 Qy 3 MIVGHHGIDIEELASIESAVTRHEGFAKVLTAQEMERPTSLKGRRIQLEYLAGRWSAKEAF 62
 Db 1 MTKGIGIDATELKRRIASMAGRQKRAFAERILTRSELDDQYELSEBKRNKFPLAGRFAKEAF 60
 Qy 63 SIKMGTGISKLGQDIEVLRNNGAPFSQPSKGKWLISLGHQDQVTAASIL 116
 Db 61 SKAWGTGIGKGVQGLQDIEVLTKEKGAPVWVANSPHNGKVFSICHTDTWAIQVLE 115
 RESULT 13
 AAM52130 ID AAM52130 standard; protein; 121 AA.
 XX AC AAM52130;
 XX DT 01-FEB-2002 (first entry)
 DB *Bacillus subtilis* ACPS.
 XX KW *Bacillus subtilis*; ACPS; acyl carrier protein synthase; active site;
 KW protein coordinate data; CoA binding site; X-ray crystallography;
 XX OS *Bacillus subtilis*.
 XX PN WO200153340-A2.
 XX PD 02-AUG-2001.
 XX PF 26-JAN-2001; 2001WO-US02732.

PR 28-JAN-2000; 2000US178639P.
 XX
 PA (AMHP) AMERICAN HOME PROD CORP.
 PA (MILL-) MILLENNIUM PHARM INC.
 XX
 PI Parris RD, Somers WS, Tam AS, Lin LL, Stahl ML;
 XX DR WPI; 2001-476201/51.
 PT Novel crystallized acyl carrier protein synthase enzyme used to
 PT identify an activator or inhibitor of a molecule or complex comprising
 PT a COA binding site, and to determine the molecular structure of a
 PT molecule or complex -
 XX disclosure; Fig 8; 181PP; English.
 CC The invention relates to a crystallized acyl carrier protein synthase
 CC (ACPS) enzyme used to identify an activator or inhibitor of a molecule or molecular
 CC complex comprising a COA binding site and to determine the molecular
 CC structure. The present sequence is that of the *Bacillus subtilis* ACPS.
 XX SQ Sequence 121 AA;
 Query Match 40.6%; Score 251; DB 22; Length 121;
 Best Local Similarity 44.6%; Pred. No. 2.9e-23; Mismatches 54;保守性 25; Indels 10; Gaps 3;
 Matches 52; Mismatches 31;保守性 25; Indels 10; Gaps 3;
 QY 3 MIVGHIDDEELASLTIASVTRHFGPAKRVLTQEMERFFSLKGARQIEYLAGRWSAKAF 62
 Db 1 MIYGIGLDITELKRKIASMGQRKAFAERLIRSEEDQYELSEKRNKNELLAGFAAKERF 60
 QY 63 SKANGTGISK-LGFQDLEVLNNERGAPY---FSQAPFSKIMLISHTDQFTAVSIL 116
 Db 61 SKAFGTGIGRQLSFDQDIEIRKDQNGKPYIICKLQSA---AVHVSITHTKEYAAQWV 116
 QY 117 E 117
 Db 117 E 117
 RESULT 14
 AAU10694
 ID AAU10694 standard; protein; 120 AA.
 XX
 AC AAU10694;
 XX
 DT 25-FEB-2002 (first entry)
 XX
 DB B. subtilis ACPS used to grow ACP/ACPS complex crystals.
 KW Crystal structure; acyl carrier protein synthase; acyl carrier protein;
 KW rational drug design method; antibiotic; 4'-phosphopantetheinyl; P-Pant;
 KW ACP/ACPS complex; protein co-ordinate data.
 XX OS *Bacillus subtilis*.
 XX WO200185743-A2.
 PN 15-NOV-2001.
 PD 26-JAN-2001; 2001WO-US02949.
 PR 08-MAY-2000; 2000US-202466P.
 PA (AMHP) AMERICAN HOME PROD CORP.
 PA (MILL-) MILLENNIUM PHARM INC.
 XX PI Parris RD, Somers WS, Tam AS, Lin LL, Stahl ML, Powers R, Xu G;
 XX DR WPI; 2002-055580/07.
 PT Crystallised complex useful in rational drug design methods, comprises

PT acyl carrier protein synthase and acyl carrier protein -
 XX
 PS Example 1; Fig 1; 147PP; English.
 XX
 CC The present invention relates to a crystallised structure comprising
 CC acyl carrier protein synthase (ACPS) complexed with acyl carrier
 protein (ACP). The invention also describes the solution structure
 CC of *Bacillus subtilis* ACP. Both these structures are useful in rational
 CC drug design methods for identifying agents that may interact with
 CC active sites of ACPS and ACP, and for testing these agents to identify
 CC agents that may represent novel antibiotics. They are also useful for
 CC design and selection of potent and selective agents which interact with
 CC ACPS and ACP, and for the design of antibiotics and other agents that
 CC interfere with 4'-phosphopantetheinyl (P-Pant) attachment, thus
 CC preventing activation of corresponding carrier proteins. The present
 CC sequence represents *B. subtilis* ACPS used to grow ACP/ACPS complex
 XX crystals.
 SQ Sequence 120 AA;
 Query Match 39.3%; Score 243; DB 23; Length 120;
 Best Local Similarity 44.1%; Pred. No. 2.8e-22; Mismatches 52;保守性 25; Indels 10; Gaps 3;
 Matches 52; Mismatches 31;保守性 25; Indels 10; Gaps 3;
 QY 6 GHGIDDEELASLTIASVTRHFGPAKRVLTQEMERFFSLKGARQIEYLAGRWSAKAF 65
 Db 3 GIGLIDITELKRIASMGQRKAFAERLIRSEEDQYELSEKRNKNELLAGFAAKERF 62
 QY 66 MGIGISK-LGFQDLEVLNNERGAPY---FSQAPFSKIMLISHTDQFTAVSIL 117
 Db 63 FGIGIGRQLSFDQDIEIRKDQNGKPYIICKLQSA---AVHVSITHTKEYAAQWV 116
 RESULT 15
 ABB47581
 ID ABB47581 standard; Protein; 118 AA.
 XX AC ABB47581;
 XX DT 05-FEB-2002 (first entry)
 XX DE Listeria monocytogenes protein #285.
 XX KW Antibacterial; gene therapy; vaccine; biosynthesis; biodegradation;
 KW vitamin B12; bacterial infection; disease.
 XX OS *Listeria monocytogenes*.
 XX PN WO200177335-A2.
 XX PD 18-OCT-2001.
 XX PR 11-APR-2001; 2001WO-FR01118.
 XX PR 11-APR-2000; 2000FR-0004629.
 XX
 PA (INSP) INST PASTEUR.
 XX
 PI Buchrieser C, Frangeul L, Couve E, Rusniok C, Fsihi H, Dehoux P;
 PI Dussurgey O, Chetouani F, Nedjari H, Glaser P, Kunst F, Cossart P;
 PI Daniels J, Goebel W, Kreft J, Kuhn M, Ng E, Vazquez-Boland JA;
 PI Dominguez-Bernal G, Garrido-Garcia P, Tierrez-Martinez A, Amend A;
 PI Chakraborty T, Domann E, Hain T, Berche P, Charbit A, Durant L;
 PI Perez-Diaz J, Baguero F, Garcia Del Portillo F, Gomez-Lopez N;
 PI Madueno E, De Pablo B, Weiland J, Kaerst U, Entian K, Hauf J;
 PI Rose M, Voss H;
 XX DR WPI; 2002-010914/01.
 XX
 PT Genomic sequence for *Listeria monocytogenes*, useful e.g. for treatment
 PT and prevention of *Listeria* and related bacterial infections, and
 PT related polypeptides -
 XX

PS Claim 6; SEQ ID No 286; 192pp; French.
XX
CC The present invention relates to the genome sequence of *Listeria*
CC monocytogenes EGD-e (see ABA03041). The genome sequence and fragments of
it are useful for selecting probes and primers for detecting genes in *L.*
CC monocytogenes and related organisms, and for studying genetic
CC polymorphisms and other genomes. The present sequence is a protein
CC encoded by the genome sequence of the present invention. Proteins
CC expressed from the genome sequence are useful for raising specific
CC antibodies, identification of *L. monocytogenes* and related organisms, and
CC for biosynthesis and biodegradation, especially biosynthesis of Vitamin
CC B12. The genome sequence and proteins encoded by it are also useful for
CC selecting compounds that regulate gene expression and cell replication
CC and modulate *L. monocytogenes*-related diseases. In addition, the genome
CC sequence and proteins encoded by it are useful in pharmaceutical and
CC vaccines compositions for the treatment or prevention of infections by *L.*
CC monocytogenes and related organisms.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp://wipo.int/pub/published_pct_sequences.
XX

SQ Sequence 118 AA;

Query Match 37.7%; Score 233; DB 23; Length 118;
Best Local Similarity 42.7%; Pred. No. 5e-21; Mismatches 35; Indels 2; Gaps 2;
Matches 50; Conservative 30; Mismatches 35; Indels 2; Gaps 2;
QY 3 MIVGHGIDIEELASIESAVTRIEHGFAKVLTKQEMERPTSLKGRQLEYLAGRWSAKEAF 62
Db 1 MIRGIGLIMIDLERVKQVEKNPFLERVLTKEIKOFEKYEGNRKIEFLAGRFAAKEAY 60
QY 63 SKAMGCGISK LGFQDLEVINNERRGAYFFSQAPPSSK-LWISIASHDQFWTASVIE 117
Db 61 AKANGTGFGKHSFTDVEILQVEDGRPHVTLVKSGENVFSITHARSAAQVIE 117

Search completed: December 10, 2003, 19:35:09
Job time : 42 secs

GenCore - version 5.1.6
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OM protein - protein search, using sw model

Run on: December 10, 2003, 19:34:21 (without alignments)

Search time 21 Seconds
245.806 Million cell updates/sec

Title: US-09-897-645-1

Perfect score: 618

Sequence: 1 MRMIVHGIDIEELASIESA.....ISHTDQFVTASVILEHENH 122

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42210858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:*

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2: /cgn2_6/ptodata/1/iaa/5B_COMBO.pep:*

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5: /cgn2_6/ptodata/1/iaa/FCITS_COMBO.pep:*

6: /cgn2_6/ptodata/1/iaa/backfilesl.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Length	DB ID	Description
1	618	100.0	122	3 US-08-997-144-2	Sequence 2, Appli
2	618	100.0	156	4 US-09-163-442-2	Sequence 2, Appli
3	289	46.8	129	4 US-09-107-532A-6990	Sequence 6990, Ap
4	251	40.6	121	4 US-09-163-446-4	Sequence 4, Appli
5	199	32.3	124	4 US-09-134-001C-4274	Sequence 4274, Ap
6	139	22.6	126	4 US-08-728-722A-10	Sequence 10, Appli
7	135	21.9	122	4 US-09-198-452A-330	Sequence 330, Appli
8	111	18.0	119	4 US-08-728-742A-11	Sequence 11, Appli
9	111	18.0	121	4 US-08-728-742A-2	Sequence 2, Appli
10	110	17.8	121	4 US-08-728-742A-3	Sequence 3, Appli
11	107	17.4	120	4 US-08-728-742A-1	Sequence 4, Appli
12	107	17.3	122	4 US-08-728-722A-4	Sequence 7, Appli
13	81	13.1	233	4 US-09-328-505-7929	Sequence 7929, Ap
14	80	13.0	208	4 US-09-134-001C-3478	Sequence 3478, Ap
15	76	12.3	130	4 US-08-728-722A-8	Sequence 8, Appli
16	74	12.0	130	4 US-08-728-722A-7	Sequence 7, Appli
17	72.5	11.7	371	4 US-09-134-001C-3672	Sequence 3672, Ap
18	72	11.7	169	4 US-09-107-532A-6366	Sequence 6366, Ap
19	71.5	11.6	130	4 US-08-728-722A-5	Sequence 5, Appli
20	71.5	11.6	431	4 US-09-107-532A-7056	Sequence 7056, Ap
21	71.5	11.6	431	4 US-09-252-931A-26219	Sequence 26219, Ap
22	70.5	11.4	318	3 US-08-680-505-3	Sequence 3, Appli
23	70.5	11.4	449	3 US-08-680-506-7	Sequence 7, Appli
24	70.5	11.4	1052	3 US-09-255-02-7	Sequence 7, Appli
25	70.5	11.4	1052	4 US-09-360-237-1	Sequence 1, Appli
26	70.5	11.4	1052	4 US-09-360-237-3	Sequence 3, Appli
27	11.0	4 US-09-107-532A-6985	Sequence 6985, Ap		

ALIGNMENTS

RESULT 1
US-08-987-144-2
Sequence 2, Application US/08987144
Patent No. 56022

GENERAL INFORMATION:

APPLICANT: Roscheck Jr., Paul R. Streptococcus Pneumoniae Gene Sequence

TITLE OF INVENTION: Streptococcus Pneumoniae Gene Sequence

NUMBER OF SEQUENCES: 3

SEQUENCE: dpg-acps

CORRESPONDENCE ADDRESS:

ADDRESSEE: Eli Lilly and Company

STREET: Lilly Corporate Center

CITY: Indianapolis

STATE: Indiana

COUNTRY: U.S.

ZIP: 46285

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/987,144

FLILING DATE: December 8, 1997

CLASSIFICATION: 424

ATTORNEY/AGENT INFORMATION:

NAME: Webster, Thomas D.

REFERENCE NUMBER: 39,872

REFERENCE/DOCKET NUMBER: X-111754

TELECOMMUNICATION INFORMATION:

TELEPHONE: 317-276-3334

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 122 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-987-144-2

Query Match: 100 %; Score 618; DB 3; Length 122;

Best Local Similarity: 100.0%; Pred. No. 6.7e-71;

Matches: 122; Conservative: 0; Mismatches: 0; Indels: 0; Gaps: 0;

QY

1 MRMIVHGIDIEELASIESA.....ISHTDQFVTASVILEHENH 120

1 MRMIVHGIDIEELASIESAVTREHEGFAKRLITAQMERFTSLKGROIEVAGRNSAKE 60

61 AFSKANGTGISKLGFQDLEVANNERGAPRFSQAPSGKWIWISHDQFVTASVILEHENH 120

61 AFSKANGTGISKLGFQDLEVANNERGAPRFSQAPSGKWIWISHDQFVTASVILEHENH 120

QY 121 ES 122
 Sequence 2, Application US/09163446
 Db 121 ES 122

RESULT 2
 US-09-163-446-2
 ; Sequence 2, Application US/09163446
 ; Patent No. 6515119
 ; GENERAL INFORMATION:
 ; APPLICANT: Fritz, Christian
 ; APPLICANT: Youngman, Philip
 ; APPLICANT: Guzman, Luz-Maria
 ; TITLE OF INVENTION: USE OF S-YDCB AND B-YDCB, ESSENTIAL BACTERIAL GENES
 ; FILE REFERENCE: 07334/097001
 ; CURRENT APPLICATION NUMBER: US/09/163, 446
 ; CURRENT FILING DATE: 1998-09-30
 ; NUMBER OF SEQ ID NOS: 12
 ; SOFTWARE: FastSEQ for Windows Version 3.0
 ; SEQ ID NO 2
 ; LENGTH: 156
 ; TYPE: PRT
 ; ORGANISM: Streptococcus pneumoniae

US-09-163-446-2

Query Match 100.0%; Score 618; DB 4; Length 156;
 Best Local Similarity 100.0%; Pred. No. 9.6e-71;
 Matches 122; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NRMIVGHGIDIEELASIESAVTRHGFANKVLTQEMERFTSLKGRQTYELAGRWSAKE 60
 Db 35 MRMIVGHGIDIEELASIESAVTRHGFANKVLTQEMERFTSLKGRQTYELAGRWSAKE 94

QY 61 AFSKANGTGTSKLGFDLVEVNERRGAPFSQAPFSKWLISHTDQFTAVSILEENH 120
 Db 95 AFSKANGTGTSKLGFDLVEVNERRGAPFSQAPFSKWLISHTDQFTAVSILEENH 154

QY 121 ES 122
 Db 155 ES 156

RESULT 3
 US-09-107-532A-6990
 ; Sequence 4, Application US/09107532A
 ; Patent No. 6583215
 ; GENERAL INFORMATION:
 ; APPLICANT: Lynn A. Doucette-Stamm and David Bush
 ; APPLICANT: Lynn A. Doucette-Stamm and David Bush
 ; TITLE OF INVENTION: NUCLEAR ACID AND AMINO ACID SEQUENCES RELATING TO
 ; NUMBER OF SEQUENCES: 7310
 ; CORRESPONDENCE ADDRESS: GENOME THERAPEUTICS CORPORATION
 ; STREET: 100 Beaver Street
 ; CITY: Waltham
 ; STATE: Massachusetts
 ; COUNTRY: USA
 ; ZIP: 23554
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: CD/ROM ISO9660
 ; COMPUTER: PC
 ; OPERATING SYSTEM: <Unknown>
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/107,532A
 ; FILING DATE: 30-Jun-1998
 ; PRIORITY APPLICATION DATA:
 ; APPLICATION NUMBER: 60/085,598
 ; FILING DATE: 14 May 1998
 ; APPLICATION NUMBER: 60/051571
 ; FILING DATE: July 2, 1997
 ; ATTORNEY/AGENT INFORMATION:

US-09-107-532A-6990

Query Match 46.8%; Score 289; DB 4; Length 129;
 Best Local Similarity 48.3%; Pred. No. 5.1e-29;
 Matches 56; Conservative 21; Mismatches 39; Indels 0; Gaps 0;

QY 3 MIVGHGIDIEELASIESAVTRHGFANKVLTQEMERFTSLKGRQTYELAGRWSAKE 62
 Db 14 MIKGIGIDAVELPRTRILIEKEPKFTARILTSDEMKLFOSLPPHRQVEFLGGRYACKEAF 73

QY 63 SKANGTGTSKLGFDLVEVNERRGAPFSQAPFSKWLISHTDQFTAVSILEENH 118
 Db 74 SKANGTGTSKLGFDLVEVNERRGAPFSQAPFSKWLISHTDQFTAVSILEENH 129

RESULT 4
 US-09-163-446-4
 ; Sequence 4, Application US/09163446
 ; Patent No. 6515119
 ; GENERAL INFORMATION:
 ; APPLICANT: Fritz, Christian
 ; APPLICANT: Youngman, Philip
 ; APPLICANT: Guzman, Luz-Maria
 ; TITLE OF INVENTION: USE OF S-YDCB AND B-YDCB, ESSENTIAL BACTERIAL GENES
 ; FILE REFERENCE: 07334/097001
 ; CURRENT APPLICATION NUMBER: US/09/163, 446
 ; CURRENT FILING DATE: 1998-09-30
 ; NUMBER OF SEQ ID NOS: 12
 ; SOFTWARE: FastSEQ for Windows Version 3.0
 ; SEQ ID NO 4
 ; LENGTH: 121
 ; TYPE: PRT
 ; ORGANISM: Streptococcus pneumoniae

US-09-163-446-4

Query Match 40.6%; Score 251; DB 4; Length 121;
 Best Local Similarity 44.6%; Pred. No. 3.2e-24;
 Matches 54; Conservative 25; Mismatches 32; Indels 10; Gaps 3;

QY 3 MIVGHGIDIEELASIESAVTRHGFANKVLTQEMERFTSLKGRQTYELAGRWSAKE 62
 Db 1 MIVGIGIDAVELPRTRILIEKEPKFTARILTSDEMKLFOSLPPHRQVEFLGGRYACKEAF 60

QY 63 SKANGTGTSKLGFDLVEVNERRGAPFSQAPFSKWLISHTDQFTAVSIL 116
 Db 61 SKAFGTGIGRQLSFQDIEBIRKDQNGKPYICLKLQA---AVHVSITHKEYAAQVVI 116

QY 117 E 117
 Db 117 E 117

RESULT 5
 US-09-134-001C-4274

Sequence 4274, Application US/09134001C

Patent No. 6380370

GENERAL INFORMATION:

APPLICANT: Lynn Doucette-Stamm et al

TITLE OF INVENTION: NUCLEAR ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS

FILE REFERENCE: GTC-007

CURRENT APPLICATION NUMBER: US/09/134, 001C

CURRENT FILING DATE: 1598-08-13

PRIORITY APPLICATION NUMBER: US 60/064, 964

PRIORITY FILING DATE: 1997-11-08

PRIORITY APPLICATION NUMBER: US 60/055, 779

NUMBER OF SEQ ID NOS: 5674

SEQ ID NO: 4274

LENGTH: 124

TYPE: PRT

ORGANISM: *Staphylococcus epidermidis*

US-09-134-001C-4274

Query Match 32.3%; Score 199.5; DB 4; Length 124; Best Local Similarity 37.2%; Pred. No. 1.2e-17; Matches 45; Conservative 30; Mismatches 41; Indels 5; Gaps 4;

QY 1 MRMIVUGHGIDIELASIESAVTRHEGFAKRVLTQEMERFTSLKG-RRQEYLAGRNSAK 59
6 IQVYGGIGTIDLIEIERIK-LQQTKEFTRILIEERIKLNQYTNERFLAGETVK 64
QY 60 EAFSKAMGTYGISK-LGFQDLEVLNNERGAPYFSQAFGGKWLISHTDQFVTAVILLE 118
Db 65 BAFSKALGIGLGKSVFQDINCYNDALGICPQDYPGFTHV-SITHVENEYAMSQVLER 122QY 119 N 119
Db 123 N 123RESULT 6
US-08-728-742A-10
; Sequence 10, Application US/08728742A.
; PATENT NO. 6579693
; GENERAL INFORMATION:
; APPLICANT: Ralph H. Lambalot, Amy M. Gehring, Ralph Reid and Christopher T. Wals
; TITLE OF INVENTION: PHOSPHOPANTETHENYL TRANSFERASES AND USES THEREOF
; NUMBER OF SEQUENCES: 78
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/728-742A
; FILING DATE: October 11, 1996
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: 60/005, 152
; FILING DATE: October 13, 1995
; APPLICATION NUMBER: 60/021, 650
; FILING DATE: July 12, 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Amy S. Mandragoras
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: HMI-015
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 42-4214
; INFORMATION FOR SEQ ID NO: 10:

SEQUENCE CHARACTERISTICS:

LENGTH: 126 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: peptide

FRAGMENT TYPE: internal

US-08-728-742A-10

Query Match 22.6%; Score 139.5; DB 4; Length 126; Best Local Similarity 30.3%; Pred. No. 5.1e-10; Matches 40; Conservative 26; Mismatches 39; Indels 27; Gaps 5;

QY 4 IVGHGIDIELASIESAVTRHEGFAKRVLTQEMERFTSLKG-RRQEYLAGRNSAK 62
3 IIGLGDIVEARIEAVIARSQDRLLRVSNDENAIWKT-HHQFVRFLAKFAKEA 60
Db 63 SKAMGTYI-SKIGFQDLEVLNNERGAPYFSQAFGGKWLISHTDQFVLER 105
Qy 61 AKAFGIGRNLGAFNQPEVFDLGPRL-----RLWGEALKLAEKLGVANMELVTLAD 113QY 106 TDQFVTAVILLE 117
Db 114 ERHYACATVIR 125RESULT 7
US-09-198-452A-330
; Sequence 330, Application US/09198452A
; PATENT NO. 6559294
; GENERAL INFORMATION:
; APPLICANT: Griffis, R.; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments of the same, and treatment of infection
; TITLE OF INVENTION: and treatment of infection
; FILE REFERENCE: 9710-003-939
; CURRENT APPLICATION NUMBER: US/09/198, 452A
; CURRENT FILING DATE: 1998-11-24
; NUMBER OF SEQ ID NOS: 6849
; SEQ ID NO: 330
; LENGTH: 122
; TYPE: PRT
; ORGANISM: *Chlamydia pneumoniae*

US-09-198-452A-330

RESULT 8
US-08-728-742A-11
; Sequence 11, Application US/08728742A
; PATENT NO. 6579695
; GENERAL INFORMATION:
; APPLICANT: Ralph H. Lambalot, Amy M. Gehring, Ralph Reid and Christopher T. Wals
; TITLE OF INVENTION: PHOSPHOPANTETHENYL TRANSFERASES AND USES THEREOF
; NUMBER OF SEQUENCES: 78
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/728,742A
 FILING DATE: October 11, 1996
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: 60/005,152
 FILING DATE: October 13, 1995
 APPLICATION NUMBER: 60/021,650
 FILING DATE: July 12, 1996
 ATTORNEY/AGENT INFORMATION:
 NAME: Amy E. Mandragoras
 REGISTRATION NUMBER: 36,207
 REFERENCE/DOCKET NUMBER: HMI-015
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (617)227-7400
 TELEFAX: (617)742-4214
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 121 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 FRAGMENT TYPE: internal
 US-08-728-742A-1
 Query Match 18.0%; Score 111.5; DB 4; Length 119;
 Best Local Similarity 32.5%; Pred. No. 1.7e-06;
 Matches 40; Conservative 22; Mismatches 40; Indels 21; Gaps 8;
 QY 6 GHGIDIEELASIESAVTRHEGFAKRVLTQEMERTSLKRRQTYELAGRWSAKEAFSKA 65
 Db 2 GVGVLVELTISIN--VENDTIERNFTPOIE-YCSAQPSVQSSF-AGTWSAKEAVFKS 56
 QY 66 MGTGISKLG---FQDLEVNNEGRGAPYF-----SQAPFSG--KIWISISHD-QFVT 111
 Db 57 L--GVKSLGGGAALKDIEVRVNKNAPAVELHGNNAKAAEAGVTDVKVSISHDDQAVA 114
 QY 112 ASV 114
 Db 115 VAV 117
 US-08-728-742A-2
 Query Match 18.0%; Score 111.5; DB 4; Length 121;
 Best Local Similarity 32.5%; Pred. No. 1.8e-06;
 Matches 40; Conservative 22; Mismatches 40; Indels 21; Gaps 8;
 QY 6 GHGIDIEELASIESAVTRHEGFAKRVLTQEMERTSLKRRQTYELAGRWSAKEAFSKA 65
 Db 2 GVGVLVELTISIN--VENDTIERNFTPOIE-YCSAQPSVQSSF-AGTWSAKEAVFKS 56
 QY 66 MGTGISKLG---FQDLEVNNEGRGAPYF-----SQAPFSG--KIWISISHD-QFVT 111
 Db 57 L--GVKSLGGGAALKDIEVRVNKNAPAVELHGNNAKAAEAGVTDVKVSISHDDQAVA 114
 QY 112 ASV 114
 Db 115 VAV 117
 US-08-728-742A-3
 Sequence 3, Application US/08/728742A
 Patent No. 6579595
 GENERAL INFORMATION:
 APPLICANT: Ralph H. Lambalot, Amy M. Gehring, Ralph Reid and Christopher T. Wals
 TITLE OF INVENTION: PHOSPHOPANTETHENYL TRANSFERASES AND USES THEREOF
 NUMBER OF SEQUENCES: 78
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: LAHIVE & COCKFIELD, LLP
 STREET: 28 State Street
 CITY: Boston
 STATE: Massachusetts
 ZIP: 02109
 COUNTRY: USA
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/728,742A
 FILING DATE: October 11, 1996
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: 60/005,152
 FILING DATE: October 13, 1995
 APPLICATION NUMBER: 60/021,650
 FILING DATE: July 12, 1996
 ATTORNEY/AGENT INFORMATION:
 NAME: Amy E. Mandragoras
 REGISTRATION NUMBER: 36,207
 REFERENCE/DOCKET NUMBER: HMI-015
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (617)227-7400
 TELEFAX: (617)742-4214
 INFORMATION FOR SEQ ID NO: 3:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 121 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 FRAGMENT TYPE: internal
 US-08-728-742A-2
 Query Match 18.0%; Score 111.5; DB 4; Length 121;
 Best Local Similarity 32.5%; Pred. No. 1.8e-06;
 Matches 40; Conservative 22; Mismatches 40; Indels 21; Gaps 8;
 QY 6 GHGIDIEELASIESAVTRHEGFAKRVLTQEMERTSLKRRQTYELAGRWSAKEAFSKA 65
 Db 2 GVGVLVELTISIN--VENDTIERNFTPOIE-YCSAQPSVQSSF-AGTWSAKEAVFKS 56
 QY 66 MGTGISKLG---FQDLEVNNEGRGAPYF-----SQAPFSG--KIWISISHD-QFVT 111
 Db 57 L--GVKSLGGGAALKDIEVRVNKNAPAVELHGNNAKAAEAGVTDVKVSISHDDQAVA 114
 QY 112 ASV 114
 Db 115 VAV 117
 US-08-728-742A-3
 Sequence 3, Application US/08/728742A
 Patent No. 6579595
 GENERAL INFORMATION:
 APPLICANT: Ralph H. Lambalot, Amy M. Gehring, Ralph Reid and Christopher T. Wals
 TITLE OF INVENTION: PHOSPHOPANTETHENYL TRANSFERASES AND USES THEREOF
 NUMBER OF SEQUENCES: 78
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: LAHIVE & COCKFIELD, LLP
 STREET: 28 State Street
 CITY: Boston
 STATE: Massachusetts
 ZIP: 02109
 COUNTRY: USA
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/728,742A
 FILING DATE: October 11, 1996
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: 60/005,152
 FILING DATE: October 13, 1995
 APPLICATION NUMBER: 60/021,650
 FILING DATE: July 12, 1996
 ATTORNEY/AGENT INFORMATION:
 NAME: Amy E. Mandragoras
 REGISTRATION NUMBER: 36,207
 REFERENCE/DOCKET NUMBER: HMI-015
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (617)227-7400
 TELEFAX: (617)742-4214
 INFORMATION FOR SEQ ID NO: 3:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 121 amino acids
 TYPE: amino acid
 TOPOLOGY: linear

MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
US-08-728-742A-3

Query Match 17.8%; Score 110; DB 4; Length 121;
Best Local Similarity 30.3%; Pred. No. 2.7e-06;
Matches 36; Conservative 19; Mismatches 48; Indels 16; Gaps 5;

Qy 8 GIDIEELASIESAVTRHGFRAKVLTAQEMERFTSLKGRRQEYLAGRWSAKEAFSKAMG 67
Db 5 GVVVEH--IDSVNIENETFVERNFTSQED--YCRKASPOSSFAGRWSAKEAVFKSL- 59

Qy 68 TGISKLG---FQDLEVLNNERGAPF-----SQAPFSG--KIVLISISTD 115
Db 60 VSSKGAGAALKDIEIGVNDANGAPVWNLHGAAAACKAQGVKQVSVSISHSQAVAV 118

RESULT 11
US-08-728-742A-1
Sequence 1, Application US/08728742A
Patent No. 6579695

GENERAL INFORMATION:
APPLICANT: Ralph H. Lambalot, Amy M. Gehring, Ralph Reid and Christopher T. Wals
TITLE OF INVENTION: PHOSPHOPANTETHINYL TRANSFERASES AND USES THEREOF
NUMBER OF SEQUENCES: 78

CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD, LLP
STREET: 28 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08-728,742A
FILING DATE: October 11, 1996

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/005,152
FILING DATE: October 13, 1995
APPLICATION NUMBER: 60/021,650
FILING DATE: July 12, 1996

ATTORNEY/AGENT INFORMATION:
NAME: Amy E. Mandragoras
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: HMT-015

TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7100
TELEFAX: (617)742-4214

INFORMATION FOR SBO ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 122 amino acids

TYPE: amino acid
TOPOLGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
US-08-728-742A-4

Query Match 17.3%; Score 107.5; DB 4; Length 122;
Best Local Similarity 32.7%; Pred. No. 5.6e-06;
Matches 40; Conservative 15; Mismatches 52; Indels 17; Gaps 6;

Qy 8 GIDIEELASIESAVTRHGFRAKVLTAQEMERFTSLKGRRQEYLAGRWSAKEAFSKAMG 67
Db 6 GVDVELVSATI--IDNETFERNFT--DTERKYCHAPNQFASPFAGRWSAKEAVFKSL- 59

Qy 68 TGISKLG---FQDLEVLNNERGAPF-----SQAPFSG--KIVLISISTD 107
Db 60 -GISKGAAAPLKDIIISSESGAPVNLHGAAKAAITAGVKSVSISHD 111

RESULT 13
US-09-328-352-7929
Sequence 7929, Application US/09328352
Patent No. 6562988

GENERAL INFORMATION:
APPLICANT: Gary L. Breton et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC99-03PA
CURRENT APPLICATION NUMBER: US/09/328, 352
CURRENT FILING DATE: 1999-06-04

A;Authors: Kraft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Ma
 ok, C.; Schlueter, T.; Simoes, N.; Terre, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland,
 C;Species: Comparative genomics of *Listeria* species
 A;Reference number: AB1077; MUID:2153729; PMID:11679669
 A;Accession: AE1185
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-118 <GLA>
 A;Cross-references: GB:NC_003210; PIDN: CAC98963.1; PID: g16410288; GSPDB: GN00177
 A;Experimental source: strain EGD-e
 C;Genetics:
 A;Gene: lmo0885
 C;Superfamily: holo-ACP synthase

RESULT 7
 AD1543
 holo-cyl-carrier protein synthase homolog lmo0884 [imported] - *Listeria innocua* (strain
 C;Species: *Listeria innocua* [strain
 C;Accession: AD1543
 C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 14-Dec-2001
 R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Blecker,
 D.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dusurget, O.; Entian, K.D.; Fsihi, H.
 Science 294, 849-852, 2001
 A;Authors: Kraft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Ma
 ok, C.; Schlueter, T.; Simoes, N.; Tierre, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland,
 A;Title: Comparative genomics of *Listeria* species
 A;Reference number: AB1077; MUID:2153729; PMID:11679669
 A;Accession: AD1543
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-118 <GLA>
 A;Cross-references: GB:AU592022; PIDN: CAC96116.1; PID: g16413334; GSPDB: GN00178
 A;Experimental source: strain Clip1262
 C;Genetics:
 A;Gene: lmo0884
 C;Superfamily: holo-ACP synthase

RESULT 8
 E89999
 holo-ACP synthase [imported] - *Staphylococcus aureus* (strain N315)
 C;Species: *Staphylococcus aureus*
 C;Accession: E89999
 C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 22-Oct-2001
 R;Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguri, A.; Mizutani-Uji, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.;
 C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.

Lancet 357, 1225-1240, 2001
 A;Title: Whole genome sequencing of methicillin-resistant *Staphylococcus aureus*.
 A;Reference number: A89758; MUID:21311952; PMID:1148146
 A;Accession: E89999
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-119 <KUR>
 A;Cross-references: GB:BA000018; PID: g13701866; PIDN: BABA43158.1; GSPDB: GN00149
 A;Experimental source: strain N315
 C;Genetics:
 A;Gene: djp
 C;Superfamily: holo-ACP synthase

RESULT 9
 F82072
 holo-(acyl-carrier-protein) synthase VC2457 [imported] - *Vibrio cholerae* (strain N1696)
 C;Species: *Vibrio cholerae* (strain
 C;Accession: F82072
 C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Feb-2001
 R;Heidelberg, J.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.
 chardson, D.; Smolava, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers,
 L.; R.R.; Metalious, J.J.; Ventter, J.C.; Fraser, C.M.
 Nature 406, 477-483, 2000
 A;Title: DNA Sequence of both chromosomes of the cholera pathogen *Vibrio cholerae*.
 A;Reference number: A82035; MUID:20406833; PMID:10952301
 A;Accession: F82072
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-126 <HEI>
 A;Cross-references: GB:AE004316; PIDN: 99657034; PIDN: AAFF95599.1; GSPDB: GNO
 A;Experimental source: serogroup O1; strain N1691; biotype El Tor
 C;Genetics:
 A;Gene: VC2457
 A;Map position: 1
 C;Superfamily: holo-ACP synthase

RESULT 10
 F71662
 holo-acyl-carrier-protein synthase (EC 2.7.8.7) RP577 - *Rickettsia prowazekii*
 C;Species: *Rickettsia prowazekii*
 C;Accession: F71662
 C;Date: 21-Nov-1998 #sequence_revision 21-Nov-1998 #text_change 03-Nov-2000
 R;Andersson, S.G.E.; Zomorodipour, A.; Andersson, J.O.; Sicheritz-Ponten, T.; Alsmark,

Nature 395, 133-140, 1998
 A;Title: The genome sequence of *Rickettsia prowazekii* and the origin of mitochondria.
 A;Accession number: A71630; NUID:99039499; PMID:9823893
 A;Status: preliminary; nucleic acid sequence not shown; translation not shown
 A;Molecule type: DNA
 A;Residues: 1-126 <AND>
 A;Cross-references: GB:AU235272; GB:AJ235269; NID:93861033; PIDN:CAA15024.1; PID:9386112
 A;Experimental source: strain Madrid E
 A;Genetics:
 A;Gene: acps; RP57
 C;Superfamily: coenzyme A; transferase
 C;Keywords: holo-ACP synthase
 A;Gene: acps
 C;Superfamily: holo-ACP synthase

Query Match 29.3%; Score 181; DB 2; Length 126;
 Best Local Similarity 37.8%; Pred. No. 1.5e-11; Indels 48; Gaps 5;
 Matches 48; Conservative 25; Mismatches 42; Indels 12; Gaps 5;
 QY 3 MIVGHGIDIBELASTESAVTRH-EGFAKRVITAQEMERFTSLKGRRQIEYLAGRNSAKEA 61
 1 MLLIGWTDIVQIPREKILNIVQERFAKILKALKEKQFTLINKNHAFLAKRPSAKEA 60
 Db 62 FSKKANGTGISK-LGFDQDLEVNERRGAP-----YFSQ-APEFSKIMWISHTQFVTA 112
 QY 61 VSKAAGVGIGGGINFRDITLNDNLGKPTWBISSHYTKLAPEN--IHLSDLDDYPICTIA 118
 Db 113 SVILEEN 119
 QY 119 FAIIESN 125

RESULT 11

B7345

holo-(acyl carrier protein) synthase - *Thermotoga maritima* (strain MSB8)
 C;Species: *Thermotoga maritima*
 C;Accession: B7345
 Garrison, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Hatt, D.H.; Hickey, C.M.; Nelson, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D.; Nature 399, 323-329, 1999
 A;Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome seq
 A;Reference number: A72200; NUID:9287316; PMID:10360571
 A;Accession: B72345
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-169 <ARN>
 A;Cross-references: GB:AB001741; GB:AB000512; NID:94981208; PIDN:AAD35774.1; PID:9498121
 A;Experimental source: strain MSB8
 C;Genetics:
 C;Gene: TM0692

RESULT 12

Query Match 27.9%; Score 172.5; DB 2; Length 169;
 Best Local Similarity 38.4%; Pred. No. 1.6e-10; Indels 48; Gaps 6;
 Matches 48; Conservative 22; Mismatches 30; Indels 25; Gaps 6;
 QY 3 MIVGHGIDIBELASTESAVTRH-EGFAKRVITAQEMERFTSLKGRRQIEYLAGRNSAKEA 62
 1 MIVGHGIDIBELASTESAVTRH-EGFAKRVITAQEMERFTSLKGRRQIEYLAGRNSAKEA 62
 Db 63 SKAMGTGIGSKLGFQDLEVNERRGAP-----YFSQAPFSKIMWISHTQFVTA 113
 53 FKAIGTGNGHSFTDVPEFLS-NGKPVLCVHKDFGFNFNYA-----HVSLSH-DRFVAL 104
 QY 114 VILEE 118
 114 VILE 117
 Db 105 WLEK 109

RESULT 12

A97810

hypothetical protein acps [imported] - *Rickettsia conorii* (strain Malish 7)

C;Species: *Rickettsia conorii*

C;Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 22-Oct-2001
 C;Accession: A97810
 R;Ogata, H.; Audic, S.; Renesto-Audiffren, P.; Fournier, P.E.; Barbe, V.; Samson, D.; Science 293, 2093-2098, 2001
 A;Title: Mechanisms of Evolution in *Rickettsia conorii* and *Rickettsia prowazekii*.
 A;Reference number: A97700; NUID:21442074; PMID:11557893
 A;Accession: A97810
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-131 <KUR>
 A;Cross-references: GB:AE006914; PIDN:AAU03419.1; PID:915619986; GSPDB:GN00173
 A;Genetics:
 A;Gene: acps
 C;Superfamily: holo-ACP synthase

Query Match 27.7%; Score 171; DB 2; Length 131;

Best Local Similarity 33.6%; Pred. No. 1.7e-10; Indels 43; Gaps 4;
 Matches 43; Conservative 31; Mismatches 42; Indels 12; Gaps 4;

QY 3 MIVGHGIDIBELASTESAVTRH-EGFAKRVITAQEMERFTSLKGRRQIEYLAGRNSAKEA 61
 1 MLLIGWTDIVQIPREKILNIVQERFAKILKALKEKQFTLINKNHAFLAKRPSAKEA 60
 Db 62 FSKKANGTGISK-LGFDQDLEVNERRGAP-----YFSQ-APEFSKIMWISHTQFVTA 112
 QY 61 VSKAAGVGIGGGINFRDITLNDNLGKPTWBISSHYTKLAPEN--IHLSDLDDYPICTIA 118
 Db 113 SVILEEN 120
 QY 119 FAIIESY 126

RESULT 13

B96960

holo-acyl-carrier protein synthase [imported] - *Clostridium acetobutylicum*
 C;Species: *Clostridium acetobutylicum*
 C;Accession: B96960
 C;Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 30-Sep-2001
 C;Accession: B96960
 R;Nolling, J.; Breenon, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee, J.; Bacteriol. 183, 4823-4838, 2001
 A;Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium *C. acetobutylicum*.
 A;Reference number: A96960; NUID:21359325; PMID:12139325
 A;Accession: B96960
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-124 <KUR>
 A;Cross-references: GB:AB001437; PIDN:AAK78469.1; PID:915023349; GSPDB:GN00168
 A;Experimental source: *Clostridium acetobutylicum* ATCC824
 C;Genetics:
 C;Gene: CAC0489
 C;Superfamily: holo-ACP synthase

Query Match 27.4%; Score 169.5; DB 2; Length 124;
 Best Local Similarity 33.9%; Pred. No. 2.3e-10; Indels 42; Gaps 3;
 Matches 42; Conservative 30; Mismatches 41; Indels 11; Gaps 3;

QY 3 MIVGHGIDIBELASTESAVTRH-EGFAKRVITAQEMERFTSLKGRRQIEYLAGRNSAKEA 62
 1 MIVGHGIDIBELASTESAVTRH-EGFAKRVITAQEMERFTSLKGRRQIEYLAGRNSAKEA 62
 Db 63 SKAMGTGIGSKLGFQDLEVNERRGAP-----YFSQAPFSKIMWISHTQFVTA 113
 59 SKALGTGFRGSFSKNNIEHKDLDGKPIVVLNGGARRAAGYGYQVQQLSISHDREKAIY 118
 QY 114 VILE 117
 Db 119 AVLE 122

RESULT 14

D81833

holo-(acyl-carrier-protein) synthase (EC 2.7.8.7) NMA2033 [imported] - *Neisseria meningitidis*

C;Species: *Neisseria meningitidis*
 C;Accession: 05-May-2000 #sequence_revision 05-May-2000 #text_change 02-Feb-2001
 R;Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morel, J.; Holloay, S.; Jageis, K.; Leather, S.; Mungall, K.; Quail, M.A.; Rajandream, A.;Title: Complete DNA sequence of a serogroup A strain of *Neisseria meningitidis* Z2491.
 A;Reference number: A81775; MUID:20222556; PMID:10761919
 A;Status: preliminary
 A;Molecule type: DNA
 A;Experimental source: serogroup A, strain 22491
 A;Gene: acps; NMA2033
 C;Superfamily: holo-ACP synthase
 C;Keywords: coenzyme A; synthase

Query Match 24.5%; Score 151.5; DB 2; Length 125;
 Best Local Similarity 33.9%; Pred. No. 1.7e-08; Gaps 4;
 Matches 43; Conservative 25; Mismatches 46; Indels 13; Gaps 4;

QY 3 MIVGHDIDELASIESAVYRHR-EGFAKVLTAQEMERITSLKRRQLEYLAGRWSAKER 61
 Db 1 MIVGHDIDELASIESAVYRHR-EGFAKVLTAQEMERITSLKRRQLEYLAGRWSAKER 61
 QY 62 FSKWKGTTG-SKUGFQDLTIVNNGAPPSQAFPSGK-----IWLISITDQFTV 111
 Db 59 FAKAVGTGIRGAVSPRNIGIHDALKPFFYAPALSKNLEEGISRYVLSMSDEEDTVL 118
 QY 112 ASVIBE 118
 Db 119 AFAVAEK 125

RESULT 15

AG0828

holo-[acyl-carrier protein] synthase (EC 2.7.8.7) [imported] - *Salmonella enterica* subsp. *Salmonella enterica* subsp. *enterica* serovar *Typhi*

A;Note: this species has also been called *Salmonella* *typhi*

C;ID: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002

C;Accession: AG0828

R;Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, T.; Connor, P.; Cronin, A.; Davis, B.; Davies, R.M.; Dowd, L.; White, N.; Farrar, S.; Moulou, S.; O'Gara, P.

Nature 413, 848-852, 2001

A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Title: Complete genome sequence of a multiple drug resistant *Salmonella enterica* serovar *Paratyphi A*. Reference number: A80502; MUID:21534947; PMID:11677608

A;Accession: AG0828

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-126 <PAB>

A;Cross-references: GB:AL513382; PIDN:CAD02779.1; PID:gi16503789; GSPDB:GN00176

A;Gene: STM2823

C;Superfamily: holo-ACP synthase

C;Keywords: coenzyme A; synthase

Query Match 24.2%; Score 149.5; DB 2; Length 126;
 Best Local Similarity 33.3%; Pred. No. 2.8e-08; Gaps 6;
 Matches 44; Conservative 24; Mismatches 37; Indels 27; Gaps 6;

QY 4 IVHGIGIDELASIESAVYRHR-EGFAKVLTAQEMERITSLKRRQLEYLAGRWSAKER 62
 Db 3 ILGIGTDPVIEARIEAVISRSGERLARRWLSDNENAWETWT-HQQPVRFLAKRFAVKEAA 60

QY 63 SKWKGTTG-SKUGFQDLTIVNNGAPPSQAFPSGKW-----LSISITD---- 107
 Db 61 AKAFGTGIRGAVSPRNIGIHDALKPFFYAPALSKNLEEGISRYVLSMSDEEDTVL 113

QY 108 - QFVTASVILLE 117

RESULT 4

DT 15-SEP-2003 (Rel. 42, Created)

[1]	RP	KW	Transferase; Lipid synthesis; Fatty acid biosynthesis; Magnesium;
	RP	STRAINE=68;	
	RA	Kasahara Y., Nakai S., Lee S., Sadaie Y., Ogasawara N.;	
	RT	"A 148 kbp sequence of the region between 35 and 47 degree of the	
	RT	Bacillus subtilis genome";	
	RT	Submitted (MBr-1997) to the EMBL/GenBank/DBJ databases.	
RN	[2]	SEQUENCE FROM N.A.	
RP	SEQUENCE FROM N.A.		
RC	STRAIN=168;		
RX	MEDLINE=98044033; PubMed=9384377;		
RA	Kunst F., Ogasawara N., Moeser I., Albertini A.M., Alloni G.,		
RA	Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchart S.,		
RA	Borruillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,		
RA	Choi S.K., Codani J.J., Comeront I.F., Cummings N.J., Daniel R.A.,		
RA	Denizot F., Devine K.M., Dusterhoff A., Ehrlich S.D., Ermelsson P.T.,		
RA	Entian K.D., Errington J., Fabret C., Ferrari E., Fouger D.,		
RA	Fritz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N.,		
RA	Ghini S.Y., Glaser P., Goffeau A., Golightly E.J., Grandi G.,		
RA	Guisepi G., Guy B.J., Haga K., Haiech J., Harwood C.R., Henaut A.,		
RA	Hilbert H., Hosappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,		
RA	Joris B., Karamata D., Kasahara Y., Klaerr-Blanchard M., Klein C.,		
RA	Kuriya K., Lapidus A., Lardinois S., Laufer J., Lazarovic V.,		
RA	Lee S.M., Levine A., Liu H., Masuda S., Mauel C., Medigue C.,		
RA	Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M.,		
RA	Noone D., O'Reilly M., Ogawa K., Ogwara A., Oudega B., Park S.H.,		
RA	Parron V., Pohl T.M., Porteille D., Porwollik S., Prescott A.M.,		
RA	Presman E., Pujic P., Purnelle B., Rapoport G., Rey M., Reynolds S.,		
RA	Rieger M., Rivolta C., Rocha E., Roche M., Sadaie Y.,		
RA	Sato T., Scanlan E., Schreiter R., Schöffe F.,		
RA	Sekiuchi J., Sekowska A., Seror P., Shin B.S., Soldo B.,		
RA	Sorokin A., Tacconi E., Takagi T., Takahashi H., Takemoto K.,		
RA	Takeuchi M., Tamakoshi A., Tanaka T., Terpstra P., Togoni A.,		
RA	Tosato V., Uchiyama S., Vandenberg M., Vannier P., Vassarotti A.,		
RA	Viari A., Wambutt R., Wedder E., Wedder H., Weitzneger T.,		
RA	Winter P., Wipat A., Yamamoto H., Yamane K., Yasumoto K., Yata K.,		
RA	Yoshida K., Yoshioka H.F., Zunstein E., Yoshioka H., Danchin A.,		
RL	RT	"The complete genome sequence of the Gram-positive bacterium Bacillus subtilis";	
RL	Nature 390:249-256 (1997)		
RL	!- FUNCTION: Transfers the 4'-phosphopantetheine moiety from coenzyme A to a Ser of acyl-carrier protein (By similarity).		
CC	!- CATALYTIC ACTIVITY: COA + apo-[acyl-carrier protein] = adenosine 3',5'-bisphosphate + holo-[acyl-carrier protein].		
CC	!- COFACTOR: Magnesium (By similarity).		
CC	!- SUBCELLULAR LOCATION: Cyttoplasmic (By similarity).		
CC	!- SIMILARITY: BELONGS TO THE P-PANT TRANSFERASE SUPERFAMILY. ACPS FAMILY.		
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CC	EMBL: AB001488; BAA19299_1; -.		
CC	EMBL: 299106; CAB12269_1; -.		
CC	PIR: H69772; H69772.		
CC	PDB: 1FLJ; 27-JUN-01.		
CC	PDB: 1FT7; 27-JUN-01.		
CC	PDB: 1F80; 15-MAY-02.		
CC	SubjList: BGG2089; acps.		
CC	HAMAP: MF_00101; -; 1.		
CC	InterPro: IPR002582; ACPS.		
CC	InterPro: IPR004568; Pantethn_trn.		
CC	Pfam: PF01648; ACPS; 1.		
CC	Protein: PDB0428; ACPS; 1.		
CC	TIGRFAMS: TIGR00515; ACPS; 1.		
CC	TIGRFAMS: TIGR00556; pantethn_trn; 1.		
CC	Best Local Similarity 44.6%; Score 251; DB 1; Length 121;		
CC	Matches 54; Conservative 25; Mismatches 32; Indels 10; Gaps 3;		
QY	3 MIVVGHIDIEETASIESAVTRHGGFAKRVLTQEMERTLSKQRQTEYLGRWSAKAF		
Db	1 MIVVGHIDIEETASIESAVTRHGGFAKRVLTQEMERTLSKQRQTEYLGRWSAKAF		
QY	63 SKANGTGTSK-LGFQDLEVLNNRERGAY---FSQRPFGKWLSTSHTDPFVTASIL		
Db	61 SKAFGTGIGRQSFQDIBIRKQDONGKPYIICRKLSQL---AVHVSITHKTEYAAQVVI		
QY	117 E 117		
Db	117 E 117		
RN	SEQUENCE FROM N.A.		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=168;		
RX	MEDLINE=98044033; PubMed=9384377;		
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RA	Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchart S.,		
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RL	RT	"The complete genome sequence of the Gram-positive bacterium Bacillus subtilis";	
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CC	!- COFACTOR: Magnesium (By similarity).		
CC	!- SUBCELLULAR LOCATION: Cyttoplasmic (By similarity).		
CC	!- SIMILARITY: BELONGS TO THE P-PANT TRANSFERASE SUPERFAMILY. ACPS FAMILY.		
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CC	EMBL: 299106; CAB12269_1; -.		
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CC	PDB: 1FLJ; 27-JUN-01.		
CC	PDB: 1FT7; 27-JUN-01.		
CC	PDB: 1F80; 15-MAY-02.		
CC	SubjList: BGG2089; acps.		
CC	HAMAP: MF_00101; -; 1.		
CC	InterPro: IPR002582; ACPS.		
CC	InterPro: IPR004568; Pantethn_trn.		
CC	Pfam: PF01648; ACPS; 1.		
CC	Protein: PDB0428; ACPS; 1.		
CC	TIGRFAMS: TIGR00515; ACPS; 1.		
CC	TIGRFAMS: TIGR00556; pantethn_trn; 1.		
QY	3 MIVVGHIDIEETASIESAVTRHGGFAKRVLTQEMERTLSKQRQTEYLGRWSAKAF		
Db	1 MIVVGHIDIEETASIESAVTRHGGFAKRVLTQEMERTLSKQRQTEYLGRWSAKAF		
QY	63 SKANGTGTSK-LGFQDLEVLNNRERGAY---FSQRPFGKWLSTSHTDPFVTASIL		
Db	61 SKAFGTGIGRQSFQDIBIRKQDONGKPYIICRKLSQL---AVHVSITHKTEYAAQVVI		
QY	117 E 117		
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CC	!- SUBCELLULAR LOCATION: Cyttoplasmic (By similarity).		
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CC	EMBL: AB001488; BAA19299_1; -.		
CC	EMBL: 299106; CAB12269_1; -.		
CC	PIR: H69772; H69772.		
CC	PDB: 1FLJ; 27-JUN-01.		
CC	PDB: 1FT7; 27-JUN-01.		
CC	PDB: 1F80; 15-MAY-02.		
CC	SubjList: BGG2089; acps.		
CC	HAMAP: MF_00101; -; 1.		
CC	InterPro: IPR002582; ACPS.		
CC	InterPro: IPR004568; Pantethn_trn.		
CC	Pfam: PF01648; ACPS; 1.		
CC	Protein: PDB0428; ACPS; 1.		
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CC	TIGRFAMS: TIGR00556; pantethn_trn; 1.		
QY	3 MIVVGHIDIEETASIESAVTRHGGFAKRVLTQEMERTLSKQRQTEYLGRWSAKAF		
Db	1 MIVVGHIDIEETASIESAVTRHGGFAKRVLTQEMERTLSKQRQTEYLGRWSAKAF		
QY	63 SKANGTGTSK-LGFQDLEVLNNRERGAY---FSQRPFGKWLSTSHTDPFVTASIL		
Db	61 SKAFGTGIGRQSFQDIBIRKQDONGKPYIICRKLSQL---AVHVSITHKTEYAAQVVI		
QY	117 E 117		
Db	117 E 117		
RN	SEQUENCE FROM N.A.		
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RC	STRAIN=168;		
RX	MEDLINE=98044033; PubMed=9384377;		
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CC	!- SUBCELLULAR LOCATION: Cyttoplasmic (By similarity).		
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CC	EMBL: AB001488; BAA19299_1; -.		
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CC	PDB: 1FLJ; 27-JUN-01.		
CC	PDB: 1FT7; 27-JUN-01.		
CC	PDB: 1F80; 15-MAY-02.		
CC	SubjList: BGG2089; acps.		
CC	HAMAP: MF_00101; -; 1.		
CC	InterPro: IPR002582; ACPS.		
CC	InterPro: IPR004568; Pantethn_trn.		
CC	Pfam: PF01648; ACPS; 1.		
CC	Protein: PDB0428; ACPS; 1.		
CC	TIGRFAMS: TIGR00515; ACPS; 1.		
CC	TIGRFAMS: TIGR00556; pantethn_trn; 1.		
QY	3 MIVVGHIDIEETASIESAVTRHGGFAKRVLTQEMERTLSKQRQTEYLGRWSAKAF		
Db	1 MIVVGHIDIEETASIESAVTRHGGFAKRVLTQEMERTLSKQRQTEYLGRWSAKAF		
QY	63 SKANGTGTSK-LGFQDLEVLNNRERGAY---FSQRPFGKWLSTSHTDPFVTASIL		
Db	61 SKAFGTGIGRQSFQDIBIRKQDONGKPYIICRKLSQL---AVHVSITHKTEYAAQVVI		
QY	117 E 117		
Db	117 E 117		
RN	SEQUENCE FROM N.A.		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=168;		
RX	MEDLINE=98044033; PubMed=9384377;		
RA	Kunst F., Ogasawara N., Moeser I., Albertini A.M., Alloni G.,		
RA	Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchart S.,		
RA	Borruillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,		
RA	Choi S.K., Codani J.J., Comeront I.F., Cummings N.J., Daniel R.A.,		
RA	Denizot F., Devine K.M., Dusterhoff A., Ehrlich S.D., Ermelsson P.T.,		
RA	Entian K.D., Errington J., Fabret C., Ferrari E., Fouger D.,		
RA	Fritz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N.,		
RA	Ghini S.Y., Glaser P., Goffeau A., Golightly E.J., Grandi G.,		
RA	Guisepi G., Guy B.J., Haga K., Haiech J., Harwood C.R., Henaut A.,		
RA	Hilbert H., Hosappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,		
RA	Joris B., Karamata D., Kasahara Y., Klaerr-Blanchard M., Klein C.,		
RA	Kuriya K., Lapidus A., Lardinois S., Laufer J., Lazarovic V.,		
RA	Lee S.M., Levine A., Liu H., Masuda S., Mauel C., Medigue C.,		
RA	Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M.,		
RA	Noone D., O'Reilly M., Ogawa K., Ogwara A., Oudega B., Park S.H.,		
RA	Parron V., Pohl T.M., Porteille D., Porwollik S., Prescott A.M.,		
RA	Presman E., Pujic P., Purnelle B., Rapoport G., Rey M., Reynolds S.,		
RA	Rieger M., Rivolta C., Rocha E., Roche M., Sadaie Y.,		
RA	Sato T., Scanlan E., Schreiter R., Schöffe F.,		
RA	Sekiuchi J., Sekowska A., Seror P., Shin B.S., Soldo B.,		
RA	Sorokin A., Tacconi E., Takagi T., Takahashi H., Takemoto K.,		
RA	Takeuchi M., Tamakoshi A., Tanaka T., Terpstra P., Togoni A.,		
RA	Tosato V., Uchiyama S., Vandenberg M., V		

QY 113 SVILE 117
 :|||
 DB 121 TVIFE 125

RESULT 15

ACPS_STAM	STANDARD;	PRT;	119 AA.
ID			
AC			
Q95SI4;			
DT	28-FEB-2003 (Rel. 41, Created)		
DT	28-FEB-2003 (Rel. 41, Last sequence update)		
DE	Holo-[acyl-carrier protein] synthase (EC 2.7.8.7) (Holo-ACP synthase)		
DE	(4'-phosphopantetheine transferase acps).		
ACPS OR DPJ OR SAV2071 OR S1875 OR MW1995,			
OS	Staphylococcus aureus (strain Mu50 / ATCC 700699),		
OS	Staphylococcus aureus (strain N313), and		
OC	Bacteria, Firmicutes; Bacillales; Staphylococcus		
OC	OX NCBI_TaxID=1588781, 158879, 196620;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RX	STRAIN_Mu50 / ATCC 700699, and N313;		
RX	MEDLINE=21311952; PubMed=11418146;		
RA	Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,		
RA	Cui L., Oguchi A., Aoki K.-I., Nagai Y., Iijan J.-Q., Ito T.,		
RA	Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A.,		
RA	Mizutani-Uji Y., Takahashi K., Sawano T., Inoue R.-I., Kaito C.,		
RA	Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,		
RA	Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,		
RA	Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.,		
RT	"Whole genome sequencing of meticillin-resistant Staphylococcus aureus",		
RT	Lancet 357:1225-1240(2001).		
RL	[2]		
RN			
RP	SEQUENCE FROM N.A.		
RC	STRAIN_MM2;		
RX	MEDLINE=22040717; PubMed=12044378;		
RA	Baba T., Takeuchi F., Kuroda M., Yuzawa H., Aoki K.-I., Oguchi A.,		
RA	Nagai Y., Iwama N., Asano K., Naimi T., Kuroda H., Cui L.,		
RA	Yamamoto K., Hiramatsu K.,		
RT	"Genome and virulence determinants of high virulence community-acquired MRSA,"		
RL	Lancet 359:1819-1827(2002).		
CC	-!- FUNCTION: Transfers the 4'-phosphopantetheine moiety from coenzyme A to a Ser of acyl-carrier protein (By similarity).		
CC	-!- CATALYTIC ACTIVITY: CoA + apo-[acyl-carrier protein] = adenosine 3',5'-bisphosphate + holo-[acyl-carrier protein].		
CC	-!- COFACTOR: Magnesium (By similarity).		
CC	-!- SUBCELLULAR LOCATION: Cyttoplasmic (By similarity).		
CC	-!- SIMILARITY: BELONGS TO THE P-PANT TRANSFERASE SUPERFAMILY. ACPS FAMILY.		
CC			
CC			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL Outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).		
CC			
DR	EMBL; AP003364; BAB5233.1; --		
DR	EMBL; AP003136; BAB43158.1; --		
DR	EMBL; AP004829; BAB95860.1; --		
DR	PIR; E89999; E89999.		
DR	HMDB; MF 00101; -- 1.		
DR	InterPro; IPR002582; ACPS.		
DR	InterPro; IPR004568; Pantethin_trn.		
DR	Pfam; PF01648; ACPS; 1.		
DR	ProDom; PDO4282; ACPS; 1.		
DR	TIGRFams; TIGR00516; acps; 1.		
DR	TIGRFams; TIGR00556; pantethin_trn; 1.		

KW Transferase; Lipid synthesis; Fatty acid biosynthesis; Magnesium; Complete proteome.
 KW MAGNESIUM (BY SIMILARITY).
 FT METAL MAGNESIUM (BY SIMILARITY).
 FT METAL MAGNESIUM (BY SIMILARITY).
 FT SEQUENCE 119 AA; 16314 MW; E2BF3CSA69657DD2 CRC64;

Query Match Best Local Similarity 37.8%; Score 208; DB 1; Length 119; Matches 45; Conservative 29; Mismatches 41; Indels 4; Gaps 3;

QY 3 MIVGGIDDEELASIESAVTRHGGPKVLTQEMERFL-KERROIEVLAGNSAKEA 61
 Db 1 MIHGIVDLEIDRKLVLYSKPKLVERLITKQKFNFTHEOKRKEILLAGRATKA 60

QY 62 PSKAMGTGTSK-LGFQDLEVLNNERRGAPPSQAFSGKWLISITDQFTAVLLEEN 119
 Db 61 FSKALGTGKGKHWAFNDICBQYDNLGKPKIDYEGFFI-VHVSISITEHYAMSQVULEKS 117

Search completed: December 10, 2003, 19:35:35
 Job time : 14 secs

Copyright (c) 1993 - 2003 Compugen Ltd.	GenCore version 5.1.6											
OM protein - protein search, using sw model												
Run on:	December 10, 2003, 19:32:36 (without alignments)											
Score:	Search time 35 Seconds											
Sequence:	1. NRMIVQHGIDIEELASIESA.....ISHTDQFVTASVILENHES 122											
Scoring table:	BLOSUM62											
Gappen:	Gapext 0.5											
Searched:	830525 seqs, 258052604 residues											
Total number of hits satisfying chosen parameters:	830525											
Minimum DB seq length:	0											
Maximum DB seq length:	200000000											
Post-processing:	Minimum Match 0%											
Listing first 45 summaries												
Database :	SPTREMBL 23;*											
1: sp_archea:*												
2: sp_bacteria:*												
3: sp_fungi:*												
4: sp_human:*												
5: sp_invertebrate:*												
6: sp_mhc:*												
7: sp_mammal:*												
8: sp_organelle:*												
9: sp_phage:*												
10: sp_plant:*												
11: sp_rabbit:*												
12: sp_virus:*												
13: sp_vertebrate:*												
14: sp_unclassified:*												
15: sp_virus:*												
16: sp_bacterioplasm:*												
17: sp_archeap:*												
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.												
SUMMARIES												
Result	Score	Query Length	DB	ID	Description					ALIGNMENTS		
No.	Score	Match	Length	DB	ID							
1	397	64.2	119	16	Q8ISF3	Q8ISF3	PRELIMINARY;	PRT;	119 AA.			
2	328.5	53.2	119	16	Q8D109	Q8D109	Q8ISF3;	DT	01-MAR-2003 (TREMBLrel. 23, Last sequence update)			
3	328.5	53.2	119	16	Q8SSK9	Q8SSK9	Q8ISF3;	DT	01-MAR-2003 (TREMBLrel. 23, Last annotation update)			
4	278.5	45.1	119	16	Q8SSK9	Q8SSK9	Q8ISF3;	DT	Putative acyl carrier protein synthase, Acps (EC 2.7.8.7). AC55 OR SMU1835.			
5	212.5	34.4	74	2	Q07122	Q07122	Q8ISF3;	DT	01-MAR-2003 (TREMBLrel. 23, Last annotation update)			
6	210.5	34.1	126	16	Q8DC72	Q8DC72	Q8ISF3;	DT	Putative acyl carrier protein synthase, Acps (EC 2.7.8.7). AC55 OR SMU1835.			
7	199.5	32.3	117	16	Q8CNR6	Q8CNR6	Q8ISF3;	DT	01-MAR-2003 (TREMBLrel. 23, Last sequence update)			
8	176	28.5	139	16	Q8D303	Q8D303	Q8ISF3;	DT	Putative acyl carrier protein synthase, Acps (EC 2.7.8.7). AC55 OR SMU1835.			
9	176	28.5	158	5	Q8MPF2	Q8MPF2	Q8ISF3;	DT	Putative acyl carrier protein synthase, Acps (EC 2.7.8.7). AC55 OR SMU1835.			
10	150.5	24.4	127	16	Q8EHT7	Q8EHT7	Q8ISF3;	DT	Putative acyl carrier protein synthase, Acps (EC 2.7.8.7). AC55 OR SMU1835.			
11	148.5	24.0	126	2	Q8FF19	Q8FF19	Q8ISF3;	DT	Putative acyl carrier protein synthase, Acps (EC 2.7.8.7). AC55 OR SMU1835.			
12	127	20.6	1858	3	P78615	P78615	Q8ISF3;	DT	Putative acyl carrier protein synthase, Acps (EC 2.7.8.7). AC55 OR SMU1835.			
13	114.5	18.5	126	16	Q8FP136	Q8FP136	Q8ISF3;	DT	Putative acyl carrier protein synthase, Acps (EC 2.7.8.7). AC55 OR SMU1835.			
14	108	17.5	153	2	Q88666	Q88666	Q8ISF3;	DT	Putative acyl carrier protein synthase, Acps (EC 2.7.8.7). AC55 OR SMU1835.			
15	107	17.3	377	3	Q96WT6	Q96WT6	Q8ISF3;	DT	Putative acyl carrier protein synthase, Acps (EC 2.7.8.7). AC55 OR SMU1835.			
16	107	17.3	1842	3	Q96WT7	Q96WT7	Q8ISF3;	DT	Putative acyl carrier protein synthase, Acps (EC 2.7.8.7). AC55 OR SMU1835.			
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45												
RN	[1]											
RP	SEQUENCE FROM N.A. STRAIN=UA159 / ATTC 700610 / Serotype C; MEDLINE=2220563; Pubmed=1239786; AJdic D., McShan W.M., McLaughlin R.E., Savic G., Chang J., Carlson M.B., Priniaux C., Tian R., Kenton S., Jia H., Lin S., Qian Y., Li S., Zhu H., Najar F., Iai H., White J., Roe B.A., Ferretti J.J.; RT "Genome sequence of Streptococcus mutans UA159, a cariogenic dental pathogen"; Proc. Natl. Acad. Sci. U.S.A. 99:14434-14439 (2002).											
RX	DR EMBL; AR015010; AN59158.1; -.											
RA	KW Transferase; Complete proteome.											
RQ	SEQUENCE 119 AA; 13218 NW; 450139C210FEBF866 CRC64;											
RT	Query Match 64.2%; Score 397; DB 16; Length 119; Best Local Similarity 62.7%; Pred. No. 2.8e-33; Matches 74; Conservative 24; Mismatches 20; Indels 0; Gaps 0;											
KW	Q8ISF3;											
QY	3 MTYGHIDIEELASIESAVTREHGFKAQVLTAGEMERTSKRRQIYLAGRWSAKF 62											
DB	1 MTYGHIDIEELASIESAVTREHGFKAQVLTAGEMERTSKRRQIYLAGRWSAKF 62											
Q96WT6	1 MIGKQDQIYDQVRAHRSRASKVLTKEELTSKRRQIYLAGRWSAKF 62											
Q96WT7	1 SKMGTGSKIGDQLEVNNEGAQPSQPSKGWLSIHTDQFTASVILENH 120											
Q96WT6	1 SKAVGGIGSLRQDIELANNKGAPITKSPPSKGNIFISHSKVNVEASVILENN 118											

RESULT 2

Q8E3MB PRELIMINARY; PRT; 119 AA.

ID Q8E3MB; PRELIMINARY; PRT; 119 AA.

AC Q8E3MB; PRELIMINARY; PRT; 119 AA.

DT 01-MAR-2003 (TREMBirel. 23, last sequence update)

DT 01-MAR-2003 (TREMBirel. 23, last annotation update)

DE Hypothetical protein.

GN GBS1729.

OS Streptococcus agalactiae (serotype III).

OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;

OC Streptococcus.

OX NCBI_TaxID=216495;

RN [1]

SEQUENCE FROM N.A.

RC STRAIN=NEM316 / Serotype III;

RX MEDLINE=22242508; PubMed=12354221;

RA Glaser P., Rusliuk C., Buchrieser C., Chevalier F., Frangeul L., Triaud-Cuot P., Msadek T., Zouine M., Couve E., Lalioui L., Poyart C., Triaud-Cuot P.,

RA Kunst F., "Genome sequence of Streptococcus agalactiae, a pathogen causing invasive neonatal disease," Mol. Microbiol. 45:1499-1513 (2002).

RL EMBL: AL766852; CAD:J73881; -.

DR Sagaloff; gbs1729; -.

KW Hypothetical protein; Complete proteome.

SEQUENCE 119 AA; 13268 MW; COEBB77DA27C5C2E CRC64;

Query Match 53.2%; Score 328.5; DB 16; Length 119;

Best Local Similarity 52.1%; Pred. No. 3.3e-26; Matches 61; Conservative 29; Mismatches 26; Indels 1; Gaps 1;

DR 62 FSKAMGTGISKLGFQDLEVINNERGAPYFSQAFSKWISISHDQFVAVS118

DR 61 YSKALGTGIGKVNFDIEILSDDKGAPLITKEPFNGKSFVSISSHGNYAOAVS117

RESULT 3

Q8DY09 PRELIMINARY; PRT; 119 AA.

ID Q8DY09; PRELIMINARY; PRT; 119 AA.

AC Q8DY09; PRELIMINARY; PRT; 119 AA.

DT 01-MAR-2003 (TREMBirel. 23, Created)

DT 01-MAR-2003 (TREMBirel. 23, Last sequence update)

DT 01-MAR-2003 (TREMBirel. 23, Last annotation update)

DE Holo-(acyl carrier-protein) synthase.

GN ACPS OR SAG168.

OS Streptococcus agalactiae (serotype V).

OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;

OC Streptococcus.

OX NCBI_TaxID=214466;

RN [1]

SEQUENCE FROM N.A.

RC STRAIN=22203 VR / Serotype V;

RX MEDLINE=22222888; PubMed=12205047;

RA Tettelin H., Masignani V., Cieslewicz M.J., Eisen J.A., Peterson S., Wessels M.R., Paulsen I.T., Nelson K.E., Margarit I., Read T.D., Maffei L.C., Wolf A.M., Beaman M.J., Brinkac L.M., Daugherty S.C., DeBoy R.T., Darkin A.S., Kolonay J.F., Madupu R., Lewis M.R., Radune D., Fedorova N.B., Scanlan D., Khouri H., Mulligan S., Carte H.A., Cline R.T., Van Aken S.E., Gill J., Scarselli M., Mora M., Iacobini E.T., Bretnon C., Galli G., Mariani M., Vugni F., Malone D., Rinaldo D., Rappuoli R., Telford J.L., Kasper D.L., Grandi G., Fraser C.M., "Complete genome sequence and comparative genomic analysis of an emerging human pathogen, serotype V Streptococcus agalactiae," Proc. Natl. Acad. Sci. U.S.A. 99:12391-12395 (2002).

DR EMBL: AEG14268; ANO0549.1; -.

DR TIGR; SAG1685; -.

Query Match 53.2%; Score 328.5; DB 16; Length 119;

Best Local Similarity 52.1%; Pred. No. 3.3e-26; Matches 61; Conservative 29; Mismatches 26; Indels 1; Gaps 1;

DR 62 FSKAMGTGISKLGFQDLEVINNERGAPYFSQAFSKWISISHDQFVAVS118

DR 61 YSKALGTGIGKVNFDIEILSDDKGAPLITKEPFNGKSFVSISSHGNYAOAVS117

RESULT 4

Q8E8K0 PRELIMINARY; PRT; 119 AA.

ID Q8E8K0; PRELIMINARY; PRT; 119 AA.

AC Q8E8K0; PRELIMINARY; PRT; 119 AA.

DT 01-MAR-2003 (TREMBirel. 23, Created)

DT 01-MAR-2003 (TREMBirel. 23, Last sequence update)

DT 01-MAR-2003 (TREMBirel. 23, Last annotation update)

DE Holo-(acyl carrier protein) synthase.

GN OB0519.

OS Oceanobacillus iheyensis.

OC Bacteria; Firmicutes; Bacillales; Oceanobacillus.

RN [1]

SEQUENCE FROM N.A.

RC STRAIN=HTE831 / DSM 14371 / JCM 11309;

RX MEDLINE=2220767; PubMed=12235376;

RA Takami H., Takaki Y., Uchiyama I., "Ridge and its unexpected adaptive capabilities to extreme environments," Nucleic Acids Res. 30:3927-3935 (2002).

DR EMBL: APO04595; BAC1255.1; -.

KW Complete proteome.

SEQUENCE 119 AA; 13474 MW; 2AF757BAAE574DE CRC64;

Query Match 45.1%; Score 278.5; DB 16; Length 119;

Best Local Similarity 47.4%; Pred. No. 4.8e-21; Matches 55; Conservative 26; Mismatches 34; Indels 1; Gaps 1;

DR 62 FSKAMGTGISKLGFQDLEVINNERGAPYFSQAFSKWISISHDQFVAVS118

DR 61 YSKALGTGIGKVNFDIEILSDDKGAPLITKEPFNGKSFVSISSHGNYAOAVS117

RESULT 5

Q8DY12 PRELIMINARY; PRT; 74 AA.

ID Q8DY12; PRELIMINARY; PRT; 74 AA.

AC Q8DY12; PRELIMINARY; PRT; 74 AA.

DT 01-JUL-1997 (TREMBirel. 04, Created)

DT 01-JUL-1997 (TREMBirel. 04, Last sequence update)

DT 01-MAR-2003 (TREMBirel. 23, Last annotation update)

DE Hypothetical 8.0 kDa protein (Fragment).

GN Lactobacillus plantarum.

OC Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae;

OC Lactobacillus.

OX NCBI_TaxID=1590;

RN [1]

SEQUENCE FROM N.A.

RC STRAIN=NCTMB826;

RX MEDLINE=9731262; PubMed=9171436;

RA Hols P., Deffrenne C., Ferain T., Derizelle S., Delplace B., Delcour J., "The alanine racemase gene is essential for growth of Lactobacillus plantarum,"

RL J. Bacteriol. 179:3804-3807 (1997).
 DR EMBL; Y00941; CAA70142.1; -.
 HSP; Q8P7T5; 1FTH.
 DR InterPro; IPR02582; ACPS.
 DR InterPro; IPR04568; Pantethin_trn.
 DR Pfam; PF01648; ACPS; 1.
 DR ProDom; PD004282; ACPS; 1.
 KW Hypothetical protein.
 FT NON TER.
 SQ SEQUENCE 74 AA; 8039 MW; 32137591876D001A CRC64;
 Best Local Similarity 34.4%; Score 212.5; DB 2; Length 74;
 Matches 41; Conservative 14; Mismatches 17; Indels 1; Gaps 1;
 QY 49 IYELAGRWSAKAEFSKAMGIGI-SKLGFQDLEVLNNERGAPYSQAFPSQKWIWISHTD 107
 1 IEFWMGRFKEAKYSKAYGIGIGAAGVQDDEILLDNAQKPEVTRHPFGPAWISHTD 60
 QY 103 QFVTVASVILEEN 120
 61 TLWMTQVILERGN 73
 DB RESULT 6
 Q8C72 PRELIMINARY; PRT; 126 AA.
 ID Q8DCT2
 AC Q8C72;
 DT 01-MAR-2003 (TREMBrel. 23, Created)
 DT 01-MAR-2003 (TREMBrel. 23, Last sequence update)
 DE Phosphotanteinehydyl transferase.
 GN VV11569.
 OS Vibrio vulnificus.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; vibionales;
 OC Vibrionaceae; Vibrio.
 OX NCBI_TaxID=672;
 RN [1] SEQUENCE FROM N.A.
 RC STRAIN=CMCP6;
 RA Rhee J.H., Kim S.Y., Chung S.S., Kim J.J., Moon Y.H., Jeong H.,
 RA Choi H.E.;
 RT "Complete genome sequence of *Vibrio vulnificus* CMCP6";
 RL Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB016802; AA009933.1; -.
 KW Transferase; Complete proteome.
 SQ SEQUENCE 126 AA; 13633 MW; 80BDE922F04B78E CRC64;
 Query Match 34.1%; Score 210.5; DB 16; Length 126;
 Best Local Similarity 42.4%; Pred. No. 5.4e-14; Mismatches 37; Indels 13; Gaps 4;
 Matches 53; Conservative 22; Mismatches 37; Indels 13; Gaps 4;
 QY 4 IVGHGIDIEELASIESAVTRH-EGFAKRVLTQAEEMERFLSKLGRQIEYLAGRWSAKF 62
 Db 3 IVGLGIDIEELASIESAVTRH-EGFAKRVLTQAEEMERFLSKLGRQIEYLAGRWSAKF 60
 QY 63 SKAMGTGISK-LGFQDLEVLNNERGAPYSQAFPSQKWIWISHTD 112
 Db 61 SKALGTGIAHGVSQDFTIKNDNDKPYQLAGRAEELAHQMGVCHTHLSLSDERHYAWA 120
 QY 113 SVILE 117
 Db 121 TVVFE 125
 DB RESULT 7
 QCNK6 PRELIMINARY; PRT; 117 AA.
 ID QCNK6
 AC QCNK6;
 DT 01-MAR-2003 (TREMBrel. 23, Created)
 DT 01-MAR-2003 (TREMBrel. 23, Last sequence update)
 DE Holo-ACP synthase.

GN SE1675.
 OS *Staphylococcus epidermidis*.
 OC Bacteria; Firmicutes; Bacillales; *Staphylococcus*.
 OX NCBI_TaxID=1282;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 1228;
 RA Zhang Y., Ren S., Li H., Fu G., Lu L., Lu G., Jia J., Tu Y., Qin Z.,
 RA Chen Z., Wen Y.,
 RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB016749; AA005274.1; -.
 KW Complete proteome.
 SQ SEQUENCE 117 AA; 13535 MW; 515246BC1C4DBDC9 CRC64;
 Query Match 32.3%; Score 199.5; DB 16; Length 117;
 Best Local Similarity 38.7%; Pred. No. 6.7e-13;
 Matches 46; Conservative 27; Mismatches 41; Indels 5; Gaps 4;
 QY 3 MIVGKGIDIBELASIESAVTRHEGAKRVLQTAQENERTS-LKGRRQIEYLAGRWSAKEA 61
 Db 1 MIYGKGIDILEIERKRN-LQNTKTERLITERDKLNOYTHEOQRLEFLAGRTVKEA 59
 QY 62 FSKANGTGISK-LGFQDLEVLNNERGAPYSQAFPSQKWIWISHTDQFETASVILEEN 119
 Db 60 FSKALGIGLGLGSVSDQDINGDALKPCIDPGYTH--SITHTENYAMSQVILEKN 116
 OS *Wigglesworthia brevipalpis*.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; *Wigglesworthia*.
 OX NCBI_TaxID=164609;
 RN [1] SEQUENCE FROM N.A.
 RP MEDLINE:2229718; PubMed=12219091;
 RA Akman L., Yamashita A., Watanabe H., Oshima K., Shiba T., Hattori M.,
 RA Akopy S.;
 RT "Genome sequence of the endocellular obligate symbiont of tsetse
 RT files, *Wigglesworthia glossinidiae*";
 RL Nat. Genet. 32:40-40 (2002).
 DR EMBL; AB063531; BAC24344.1; -.
 KW Complete proteome.
 SQ SEQUENCE 139 AA; 15871 MW; CD9084121DCP897 CRC64;
 Query Match 28.5%; Score 176; DB 16; Length 139;
 Best Local Similarity 36.2%; Pred. No. 2.2e-10;
 Matches 47; Conservative 23; Mismatches 46; Indels 14; Gaps 4;
 QY 4 IVGHGIDIEELASIESAVTRH-EGFAKRVLTQAEEMERFLSKLGRQIEYLAGRWSAK 59
 Db 3 IVGLGIDIEELASIESAVTRH-EGFAKRVLTQAEEMERFLSKLGRQIEYLAGRWSAK 62
 QY 60 EAESKAMGTGISK-LGFQDLEVLNNERGAPYSQAFPSQKWIWISHTDQFETASVILEEN 119
 Db 63 EAASKAFGLGMKGKLYFSQFEVINNLNGKPYFENNTAKNLTNINHLSLDERHYAWA 122
 QY 110 VTVASVILEEN 119
 Db 123 ACATVVFEDN 122

RESULT 9
 Q8ANP2 PRELIMINARY; PRT; 158 AA.
 ID Q8ANP2
 AC Q8ANP2

DT 01-OCT-2002 (TREMBrel. 22, Created)
 DT 01-OCT-2002 (TREMBrel. 22, Last sequence update)
 DT 01-MAR-2003 (TREMBrel. 23, Last annotation update)
 DE Hypothetical protein
 OS Dictyostelium discoideum (Slime mold)
 OC Eukaryota; Mycota; Dictyosteliida; Dictyostelium
 OX NCBI_TaxID:44639;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=AX4;
 RA Gloeckner G., Bichinger L., Szafranski K., Pachebat J., Dear P.,
 RA Lehmann R., Baumgart C., Parra G., April J.F., Guigo R., Kumpf K.,
 RA Tunggal B., Cox B., Quail M.A., Platzer M., Rosenthal A., Noegel A.A.,
 RT "Sequence and Analysis of Chromosome 2 of Dictyostelium";
 RL Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AC:116961; AAM:37651; -.
 DR InterPro; IPR002582; ACPS.
 DR InterPro; IPR004568; Paratethn_trn.
 DR ProDom; PPD04282; ACPS; 1.
 DR TIGRFAMS; TIGR0516; acps; 1.
 DR Hypothetical protein; 1.
 KW TIGRFAMS; TIGR0516; paratethn_trn; 1.
 SQ SEQUENCE 158 AA; 17931 MW; A4E56FBF387B08EB CRC64;
 Query Match 28.5%; Score 176; DB 5; Length 158;
 Best Local Similarity 30.7%; Pred. No. 2.6e-10; Indels 48; Gaps 5;
 Matches 50; Conservative 21; Mismatches 44; Indels 48; Gaps 5;
 QY 1 MRMIVSHGIDTEELASIESAVTRHGRKAVLTAQEMERFTSL----- 43
 Db 1 MNKIFGIGNDIVKISKILESSF-----KRAFNEVVISIFKSINLPASITFESIDDDNNE 53
 QY 44 -----KGRRIQEVYLAGRWSAKEAFSKAMGT-GISKLGFDQLEVNNERGAP 88
 Db 54 LNNNNNNNNNNNNNNNNRGEFLVLAGHWAKEISYKRAIGNQDRSKUNFQNIQILNESNGRP 113
 QY 89 YF----SQAPFS---GKWLISIHTDQFTASVILEHENES 122
 Db 114 YVNLLTEESYKELGINKHILASHEPDYAIINVILESNEST 156
 RESULT 10
 ID Q8EH77 PRELIMINARY; PRT; 127 AA.
 ID Q8EH77; PRELIMINARY; PRT; 127 AA.
 DT 01-MAR-2003 (TREMBrel. 23, Created)
 DT 01-MAR-2003 (TREMBrel. 23, Last sequence update)
 DT 01-MAR-2003 (TREMBrel. 23, Last annotation update)
 DE Holo-(acetyl-carrier protein) synthase
 ACPS OR_So1352.
 OS Shewanella oneidensis.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Alteromonadales; Shewanella.
 OC NCBI_TaxID:70863;
 RN [1]
 RP SEQUENCE FROM N.A.
 SQ SEQUENCE 126 AA; 14152 MW; 4D0738210F742AFF CRC64;
 Query Match 24.4%; Score 150.5; DB 16; Length 127;
 Best Local Similarity 37.6%; Pred. No. 8.4e-08; Indels 22; Mismatches 43; Indels 13; Gaps 6;
 Matches 47; Conservative 22; Mismatches 43; Indels 13; Gaps 6;
 QY 4 IVGHGIDIEELASIESAVTRH-EGAKRVLTAQEMERFTSLKGRRIQEVYLAGRWSAKEAF 62
 Db 3 TIGLGDIVELAERIKAVIARSGERLARRVLSNEWBIWKT--HHQPVRFKRAFVKEA 60
 QY 63 SKAMFTGI-SKGFPDQLEVNNERGAPYSQAPFSKIN-----LISH 105
 Db 61 AKAFGFGIRGNGLAFNQFEVENDELKPRL---RLWSEALKLAEKLGVNMHVTLD 113
 RESULT 12
 ID P78615 PRELIMINARY; PRT; 1858 AA.
 ID P78615; PRELIMINARY; PRT; 1858 AA.
 AC P78615; PRELIMINARY; PRT; 1858 AA.
 AC P78615; PRELIMINARY; PRT; 1858 AA.
 DT 01-MAY-1997 (TREMBrel. 03, Created)
 DT 01-MAY-1997 (TREMBrel. 03, Last sequence update)
 DT 01-MAR-2003 (TREMBrel. 23, Last annotation update)
 DE Fatty acid synthase, alpha subunit.
 ACPS.
 OS Emericella nidulans (Aspergillus nidulans).

OC	Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC	Bacilli; Trichocomaceae; Enterocella.
RN	SEQUENCE FROM N.A.
RX	NCBI_TAXID=162425;
[1]	
RX	SEQUENCE FROM N.A.
RX	MEDLINE:97121482; PubMed=8962148;
RT	"Aspergillus" has distinct fatty acid synthases for primary and secondary metabolism.";
RL	Proc. Natl. Acad. Sci. U.S.A. 93:14873-14877 (1996).
DR	EMBL; U75347; AACB1493.1; -.
DR	HSPP; Q9P75; 1FTF.
DR	InterPro; IPR02582; ACPS.
DR	InterPro; IPR00794; Ketoacyl-synth.
DR	InterPro; IPR01568; Pantethin_trn.
DR	InterPro; IPR06162; Pantethein_attach.
PFAM	PF01648; ACPS; 1.
PFAM	PF00109; ketoacyl-synth; 1.
PFAM	PF2801; ketoacyl-synt_C; 1.
DR	Prodrom; PD004282; ACPS; 1.
DR	TIGRFAMS; TIGR00556; Pantethin_trn; 1.
DR	PROSITE; PS00606; B_KETOCACIL_SYNTHASE; 1.
KW	PROSITE; PS00012; PHOSPHOPANTETHINE; 1.
SEQUENCE	1858 AA; 204730 MW; 3D961E8716C9E24D CRC64;
Query Match	20.6%; Score 127; DB 3; Length 1858;
Best Local Similarity	34.2%; Pred. No. 0.00071;
Matches	40; Conservative 18; Mismatches 45; Indels 14; Gaps 5;
QY	8 GIDIEELASIESAVTRHFGFAKRVLTAGEMERFTSLKGRQRQIBYLAGRNSAKEAFFSKANG 67
DB	1744 GIVDVE--SIDSINISNTERIILPASEQQYCONAPSQ-SSPAGRNSAKEAVFKSLG 1798
QY	68 TGJISKLG--FQDIEVLVNNERGAYF----SQDPFSG--KIMWISHTDQFVTAIVI 115
DB	1799 VCKKGAGAFLKQDIEVLEIENDNSGAPTHGAAEAKKEAGYKHISISSIONDMQAVAVI 1855
RESULT	13
Q8P136	
ID	Q8P136 PRELIMINARY; PRT; 126 AA.
AC	Q8P136; 01-MAR-2003 (TREMBrel. 23, Created)
DT	01-MAR-2003 (TREMBrel. 23, Last sequence update)
DT	01-MAR-2003 (TREMBrel. 23, Last annotation update)
DE	Phosphopantetheinyl transferase (EC 2.7.8.7).
GN	ACPS; ORI LA302
OC	Bacteri; Spirochaetes; Spirochaetales; Leptospiraceae; Leptospira.
OX	NCBI_TaxID=173;
RN	[1]
RP	SEQUENCE FROM N.A.
RC	STRAIN=56601 / Serogroup Icterohaemorrhagiae / Serovar Iai;
RA	Ren.S.;
RL	Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR	EMBL; AE011490; ANN50500.1; -.
KW	Transfase; Complete proteome.
SQ	SEQUENCE 126 AA; 14419 MW; F7C32E3F9C289785 CRC64;
Query Match	18.5%; Score 114.5; DB 16; Length 126;
Best Local Similarity	32.0%; Pred. No. 0.00043;
Matches	41; Conservative 23; Mismatches 47; Indels 17; Gaps 6;
RESULT	15
P8866	
ID	P78866 PRELIMINARY; PRT; 377 AA.
AC	P78866; 01-MAY-1997 (TREMBrel. 03, Created)
DT	01-JAN-1998 (TREMBrel. 05, Last sequence update)
DT	01-MAR-2003 (TREMBrel. 23, Last annotation update)
DB	Unknown protein (Fragment).
OS	Schizosaccharomyces pombe (Fission yeast);
OC	Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes; Schizosaccharomyces pombe; Schizosaccharomyctales; Schizosaccharomycetaceae;
OC	Schizosaccharomyctales; Schizosaccharomycetaceae;
OC	NCBI_TaxID=4896;
RP	SEQUENCE FROM N.A.
RN	[1]
RC	STRAIN=PR745;
RX	MEDLINE=98162722; PubMed=9501991;
RA	Yoshioka S.; Kato K.; Nakai K.; Okayama H.; Nojima H.;
RT	"Identification of open reading frames in Schizosaccharomyces pombe" ;
RT	CDNA Res. 4:363-369 (1997).
RL	Prodrom; DR0916; PN120771;

